



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115431

TO: Diana Johannsen
Location: REM/2C85
Art Unit: 1634
Monday, March 01, 2004

Case Serial Number: 09692077

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Johannsen,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

```
Run on:      February 29, 2004, 20:07:24 ; Search time 870 Seconds
              (without alignments)
              2540.799 Million cell updates/sec
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Title: US-09-692-077D-1_COPY_880_930

Perfect score: 51

Sequence: 1 gagggaacgagctgaaagagga...agggagggagggaggaagagctgc 51

Scoring cable: IDENTITY_NUC

Gapor 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 150 summaries

Database :

1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pac.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_eb.*
12: gb_ey.*
13: gb_un.*
14: gb_vt.*
15: en_ba.*
16: en_fun.*
17: en_hum.*
18: en_in.*
19: en_in.*
20: en_om.*
21: en_ot.*
22: en_ov.*
23: en_pat.*
24: en_ph.*
25: en_pl.*
26: en_ro.*
27: en_sts.*
28: en_un.*
29: en_vt.*
30: en_hg_hum.*
31: en_hg_inv.*
32: en_hg_other.*
33: en_hg_hum.*
34: en_hg_pln.*
35: en_hg_rnd.*
36: en_hg_mam.*
37: en_hg_vit.*
38: en_hg_vt.*
39: en_hgo_hum.*
40: en_hgo_mus.*
41: en_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	885	9	HUMA2C22	M38742 Human alpha
2	51	100.0	1030	9	HSA325747	AJ355747 Homo sapi
3	51	100.0	1353	6	AX350489	AJ355048 Sequence
4	51	100.0	2072	6	AR270618	AR270618 Sequence
5	51	100.0	2072	9	HXMADRA2RA	M34041 Human alpha
6	51	100.0	3274	6	AX548756	AX548756 Sequence
7	51	100.0	9944	9	AF005900	AF005900 Homo sapi
8	43.6	85.5	133405	10	AL662790	AL662790 Mouse DNA
9	43.6	85.5	216444	2	AC069060	AC069060 Mus muscu
10	43.4	87.1	1185	10	ASP437259	AJ427259 Anomalur
11	43.2	84.7	1183	4	OCARAB	Y15946 Oryzocolagus
12	43.2	84.7	1183	4	OCY16189	Y16189 Oryzocolagus
13	43.2	84.7	206933	2	AC108794	AC108794 Mus muscu
14	43.2	84.7	215065	2	AC103291	AC103291 Rattus no
15	43.2	84.7	222507	2	AC112440	AC112440 Rattus no
16	43.2	84.7	226214	2	AC126653	AC126653 Rattus no
17	43.2	84.7	287497	2	AC106946	AC106946 Rattus no
18	43.2	84.7	293183	2	AC095903	AC095903 Rattus no
19	43	84.3	1191	10	CCAA437260	AJ327260 Castor ca
20	42.6	83.5	217323	2	AC115724	AC115724 Mus muscu
21	42.6	83.5	232202	2	AC115740	AC115740 Mus muscu
22	42.2	82.7	31533	10	BX465209	BX465209 Mouse DNA
23	42.2	82.7	186272	10	AL672046	AL672046 Mouse DNA
24	42.2	82.7	189624	2	AC128836	AC128836 Rattus no
25	42.2	82.7	189886	2	AC128302	AC128302 Rattus no
26	42.2	82.7	230127	10	AL691481	AL691481 Mouse DNA
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28	42.2	82.7	230313	2	AC120625	AC120625 Rattus no
29	42.2	82.7	268151	2	AC111391	AC111391 Rattus no
30	42	82.4	1198	4	ECNAR2B	Y15945 Equus cabal
31	42	82.4	185321	2	AC110324	AC110324 Rattus no
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39	41.6	81.6	30837	2	AC126874_4	Conjunction (5 of
40	41.6	81.6	42003	2	AC145716	AC145716 Homo sapi
41	41.6	81.6	42920	2	AC145702	AC145702 Homo sapi
42	41.6	81.6	49999	6	AX015902	AX015902 Sequence
43	41.6	81.6	49999	6	AX015908	AX015908 Sequence
44	41.6	81.6	68233	6	AX695956	AX695956 Sequence
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47	41.6	81.6	117612	10	AL591365	AL591365 Mouse DNA
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49	41.6	81.6	122436	10	AB051897	AB051897 Mus muscu
50	41.6	81.6	136171	2	AC141946	AC141946 Rattus no
51	41.6	81.6	138191	8	BX842634	BX842634 Neurospor
52	41.6	81.6	141458	2	AC142044	AC142044 Rattus no
53	41.6	81.6	149814	10	AC130838	AC130838 Mus muscu
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56	41.6	81.6	153228	2	AC139129	AC139129 Mus muscu
57	41.6	81.6	154216	2	AC120503	AC120503 Didelphis
58	41.6	81.6	155094	2	AC122080	AC122080 Rattus no
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62	41.6	81.6	160517	10	AC132292	AC132292 Mus muscu
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65	41.6	81.6	167787	2	AC109761	AC109761 Rattus no

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C	73	41.6	81.6	177675	10	AC124534	AC124534 Mus muscu
C	74	41.6	81.6	178449	2	AC128251	AC128251 Mus muscu
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C	77	41.6	81.6	185568	9	AC105227	AC105227 Homo sapi
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C	79	41.6	81.6	187252	10	AL607109	AL607109 Mouse DNA
C	80	41.6	81.6	189858	2	AC122382	AC122382 Mus muscu
C	81	41.6	81.6	191338	2	AC127650	AC127650 Rattus no
C	82	41.6	81.6	192164	2	AC140220	AC140220 Mus muscu
C	83	41.6	81.6	193035	2	AC125186	AC125186 Mus muscu
C	84	41.6	81.6	194614	2	AC113594	AC113594 Mus muscu
C	85	41.6	81.6	196383	2	AC113594	AC113594 Mus muscu
C	86	41.6	81.6	197295	2	AC139652	AC139652 Rattus no
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C	89	41.6	81.6	199593	2	AL808137	AL808137 Mouse DNA
C	90	41.6	81.6	202634	2	AC102541	AC102541 Mus muscu
C	91	41.6	81.6	205633	10	AL591496	AL591496 Mouse DNA
C	92	41.6	81.6	206472	2	AC131874	AC131874 Rattus no
C	93	41.6	81.6	207283	2	AC131874	AC131874 Rattus no
C	94	41.6	81.6	207450	2	AC133253	AC133253 Rattus no
C	95	41.6	81.6	210092	10	AC126505	AC126505 Mus muscu
C	96	41.6	81.6	210386	10	AL663065	AL663065 Mouse DNA
C	97	41.6	81.6	211237	2	AC138325	AC138325 Mus muscu
C	98	41.6	81.6	211873	10	AL596122	AL596122 Mouse DNA
C	99	41.6	81.6	212115	2	AC105773	AC105773 Mus muscu
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C	109	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	110	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
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C	115	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	116	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	117	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	118	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	119	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	120	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	121	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	122	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
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C	126	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
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C	128	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	129	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	130	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	131	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	132	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	133	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	134	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
C	135	41.6	81.6	220331	2	AC128616	AC128616 Rattus no
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139	41.6	81.6	241629	2	AC097388	AC097388 Rattus no
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142	41.6	81.6	243252	2	AC120850	AC120850 Mus muscu
143	41.6	81.6	243366	2	AC115313	AC115313 Rattus no
144	41.6	81.6	244388	2	AC132065	AC132065 Rattus no
145	41.6	81.6	244455	2	AC121672	AC121672 Rattus no
146	41.6	81.6	247180	2	AC108653	AC108653 Rattus no
147	41.6	81.6	247504	2	AC113220	AC113220 Rattus no
148	41.6	81.6	247686	2	AC111776	AC111776 Rattus no
149	41.6	81.6	248458	2	AC105827	AC105827 Rattus no
150	41.6	81.6	249122	2	AC135438	AC135438 Rattus no

ALIGNMENTS

RESULT 1	HUMA2C2	885 bp	DNA	linear	PRI 06-MAR-1995
LOCUS	HUMA2C2				
DEFINITION	Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.				
ACCESSION	M38742.1				
VERSION	M38742.1				
KEYWORDS	alpha-2 adrenergic receptor.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	Chang, A.C., Ho, T.F., and Chang, N.C.				
TITLE	In vitro amplification by polymerase chain reaction of a partial human alpha-2 adrenergic receptor in				

biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)

Original source text: Human adult neuroblastoma DNA, clone PCRA2.

Draft entry and computer-readable sequence for (Unpublished (1990))

by A.C. Chang, 20-SEP-1990.

Institute of Neuroscience

155, Sect II, Li-Neon St.

Taipei, Taiwan, 11221 ROC.

Location/Qualifiers

1. 885

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="4p16.3-p15"

/clone="PCRA2"

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/tissue_type="neuroblastoma"

/dev_stage="adult"

1. 885

/gene="ADRA2C"

1. 885

/gene="ADRA2C"

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/protein_id="AA462823.1"

/db_xref="GI:1177868"

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/translation="FCTSSIVLCAISIDRYWVSRALVNSKTPRRICITLTVWL

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ENKEETPEDTPTALPSPMALNRSGGQGEVCAAPDEDAEEREEEREEEREP

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ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 885;

Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
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Db 598 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 648

RESULT 2
HSA325747/c 1030 bp DNA linear PRI 18-JUL-2002
LOCUS HSA325747
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NB1-8185.
ACCESSION AJ325747
VERSION AJ325747.1 GI:15870141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1030)
AUTHORS Kurumaji, A.S., Gizaullin, R.Z., Al-Amin, A.N., Wang, F., Kvasna, S.M.,
Podewski, R.M., Matushkin, Y.G., Gyanchandani, A., Mutsaers, O.V.,
Levitky, V.G., Kolchanov, N.A., Protodopov, A.I., Kaashub, V.I.,
Kiselev, L.L., Wasserman, W., Mahlestedt, C. and Zabarovsky, E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 1030)
AUTHORS Zabarovsky, E.R.
TITLE Direct Substitution
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumourbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
source 1..1030
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NB1-8185"

ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
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Db 199 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 149

RESULT 3
AX350489 1353 bp DNA linear PAT 06-FEB-2002
LOCUS AX350489
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
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Db 880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 4
AR270618 2072 bp DNA linear PAT 10-APR-2003
LOCUS AR270618
DEFINITION Sequence 1181 from patent US 6500938.
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-DEC-2002;
FEATURES
source location/Qualifiers
1..2072
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
|||||
Db 1292 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342

RESULT 5
HUMADRA2RA 2072 bp DNA linear PRI 30-OCT-1994
LOCUS HUMADRA2RA
DEFINITION Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
ACCESSION M34041
VERSION M34041.1 GI:178197
KEYWORDS alpha-2-adrenergic receptor; plasma membrane protein;
receptor-coupled G protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
TITLE Expansion of the alpha 2-adrenergic receptor family: cloning and
characterization of a human alpha 2-adrenergic receptor subtype,
the gene for which is located on chromosome 2
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
MEDLINE 90311349
PUBMED 2164221
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for (1) kindly submitted
by J.W.Lomasney, 03-MAY-1990, for release after publication.
FEATURES
source location/Qualifiers
1..2072
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="2"
gene 413..1765
CDS 413..1765

[illegible]

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	Burner,G.C., Roush,C.L. and Brown,J.P. Antigenic peptides such as for G protein-coupled receptors (GPCRs), antihodis thereto, and systems for identifying such antigenic peptides Patent: WO 02061087-A 41-08-AUG-2002; Lifespan Biosciences, Inc. (US) Location/Qualifiers 1..3274
JOURNAL	
FEATURES	
SOURCE	

Query Match	100.0%;	Score 51;	DB 6;	Length 3274;
Best Local Similarity	100.0%;	Pred. No.	0.0016;	
Matches	51;	Conservative	0.0016;	

[illegible]

RESULT 7	AF005900	9944 bp	DNA linear	PR1 05-AUG-2003
LOCUS	AF005900			
DEFINITION	Homo sapiens	alpha2B-adrenergic receptor (alpha2C2NR) gene,		
ACCESSION	AF005900	complete cds.		
VERSION	AF005900.2	GI:33435705		
KEYWORDS	.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			

Homo sapiens (human)
 Homo sapiens
 Hukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/clone_lib="brain fetal genomic library"
5500..6852
/gene="alpha2C2AR"
/note="alpha2C2R adrenergic receptor gene"
5500..6852
CDS

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pol_ya_signal
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/db_xref="GI:22456258.1"
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KQPRDHGQALASAKTLPALASVAREVNHSSCSSTKEGEGTPEDTGRALPMAA
LNSGQGGQEGVCGASPDEABEEEEEEEEEEBEEBEEBEEBEEBEEBEEBEEBEEB
VLTATRGQVILGRGVACIGGQMMRRRLTRERFTFVAVIAGVFTLCMPDFFTSY
LQALCPKCKVPHCLPQFFMWISYCNSSLNPIVYITFNDDPRARRLCLCPMTQTAM
8751. .8756

Query Match	100.0%;	Score 51;	DB 9;	Length 9944;
Best Local Similarity	100.0%;	Pred. No. 0.0015;		
Matches	51;	Conservative	0;	Mismatches 0

[illegible]

RESULT 8	
AL662790	
LOCUS	
DEFINITION	
Accession	Mouse DNA sequence from clone RP23-53E3 on chromosome 11, complete
Version	AL662790
Keywords	HTG.
Source	Mus musculus (house mouse)
Organism	Mus musculus (house mouse)

REFERENCE
Bukacina, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scleroglossa; Muridae; Mus Smith, M.
TITLE
Direct Submission
Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

LSSSLGSFFVPCIMILVYIRYLIAKRSRRRGRAGGSGEESRQACVPCGSPAS
AKIPLTLATPVASASEANGSPSKAGEKEEGTPEDPQTALPGMATLPSNGQQKEV
SGSLSEAEAEHEEEHEEEDBPQAVPSPVSPSLPQQGSRYLATLTAGQVLVNG
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L^P"

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/organism="Oryctolagus cuniculus"
/mol_type="genomic DNA"
/db_xref="taxon:9986"
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CDS

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Matches	45; Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Oy	1 GAGGATTAAGCTGTAAGAGAGAAAGAGAGAGAGAGAGAAGAG	48						
Dd	845 GAGGAATAACTGTAAAGAGAGAGAGAGAGAGAGAGAGAGACGAG	892						
RESULT 13								
ACI08794/c	ACI08794	206933 bp	DNA	linear	HTG 22-OCT-2002			
LOCUS	Mm musculus clone RP23-59D8, WORKING DRAFT SEQUENCE, 10 ordered pieces.							
DEFINITION								
ACCESSION	ACI08794							
VERSION	ACI08794.4	GI:24211386						

KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 206933)
AUTHORS
Birren, B., Nusbaum, C. and Lander, E.
TITLE
Mus musculus, clone RP23-59D8
JOURNAL
Unpublished

REFERENCE	AUTHORS
2 (bases 1 to 206933)	
	Blitten,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barina,N., Bastien,Y., Boguslavsky,L., Boukanger,B., Brown,A., Camarata,J., Campioano,A., Chang,J., Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Gage,S., Gordon,S., Goyette,M., Gram,L., Grand-Pierre,N., Hinds,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karacas,A., Kells,C., Labocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,U., Marguis,N., Matthews,C., McCarthy,M., McKean,P., McKernan,K., Meldiri,J., Menus,L., Mohya,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rossetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strassan,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triggillo,T., Vassiliou,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE	Direct Submission
JOURNAL	Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE
AUTHORS

3 (bases 1 to 206933)

Birren, B., Nusbach, C., Iander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boughalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-pierre, N., Haez, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Milnova, T., Mieneva, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norby, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhngam, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,

Paetecnek, S., Paul, H., Perez, A., Perez, L., Frankoch, C.,
 Plopper, F., Poidexter, A., Popovic, D., Pittme, E., Pu, L.-L.,
 Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
 Rives, C., Rodey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
 Sanders, W., Savery, G., Scheier, S., Scott, G., Shatsman, S., Shen, H.,
 Shetty, J., Shvartbeyn, A., Sleson, I., Sitter, C.D., Smaj, D.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sotelle, R., Soe, J.,
 Steime, M., Strong, R., Sutton, A., Swatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, D., Tingley, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villaena, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Medendorp, A., Weiser, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 215065)
 Worley, K.C.
 Direct Submission
 Submitted (24-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 215065)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 9, 2002 this sequence version replaced gi:23268227.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsa.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsa.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GJSTU
 Center clone name: CH230-13104
 ----- Summary Statistics
 Assembly program: Phrap, version 0.990329
 Consensus quality: 200859 bases at least Q40
 Consensus quality: 202934 bases at least Q30
 Consensus quality: 204251 bases at least Q20
 Estimated insert size: 207073; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsa.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 211244: contig of 211244 bp in length
 * 211245 211344: gap of unknown length

Guaratene, P., Haland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hollins, B., Hollins, B., Howells, S., Huylk, S., Hume, J., Idelbird, D., Jackson, A., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kows, C., Kraft, C.L., Lebow, H., Levin, D., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, M., Liu, Y., London, P., Longacre, S., Lopez, J., Lornshewer, L., Louisedge, H., Lozato, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindradevi, M., Mahmood, M., Malloy, K., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawliny, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muniasa, M., Murphy, M., Nakkeris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokilemeh, O., Okumu, G., Olamposagoun, A., Pal, S., Parke, K., Paeterak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plöpper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachin, I., Reeves, K., Reiser, M.A., Relph, R., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Riggs, F., Sanders, W., Savery, G., Scheerer, S., Scott, G., Shatman, S., Shiety, J., Shvartbeyn, A., Sismon, I., Sitter, C.D., Smadys, D., Speed, A., Sodergren, E., Song, X.-Z., Sorrell, R., Sosai, J., Steine, R., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, T., Thomas, N., Thomas, S., Thigey, A., Trejos, Z., Umanik, C., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wleciuk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhu, D., von Weizsäcker, G., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Wetters, G., and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 222507)
Worley, K.C.

Direct Submission
Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:22856702, and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described assembly (a "contig-scaffold"). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GRIP
Center clone name: CH230-144K15
----- Summary Statistics
Assembly program: Phrap; Version 0.990329
Consensus quality: 206932 bases at least Q40
Consensus quality: 206448 bases at least Q30
Consensus quality: 209801 bases at least Q20

Estimated insert size: 210499; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases, sum-of-contigs estimation

* (see <http://edlib.bic.ac.uk/ncbi/blast/blast.cgi>)
 * NOTE: This is a working draft sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preffered.

FEATURES	source
53077:	contig of 53077 bp in length
53176:	gap of unknown length
53198:	contig of 4221 bp in length
57398:	gap of unknown length
57498:	gap of unknown length
164797:	contig of 107299 bp in length
164897:	gap of unknown length
164898:	gap of unknown length
225057:	contig of 57610 bp in length.
Location/Qualifiers	

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Query Match	84.7%	Score 43.2;	DB 2;	Length 222507;
Best Local Similarity	93.8%	Pred. No. 0.11;		
Matches	45;	Conservative		

	Conservative	Mismatches	Indels	Gaps
QY	1	3	0	0
Db	15374	48	0	0

RESULT 16					
AC126653					
LOCUS	AC126653	226214 bp	DNA	linear	HTG_13-MAY-2003
DEFINITION	Rattus norvegicus clone CH230-236K3,				
	unordered pieces.				
ACCESSION	AC126653				
VERSION	AC126653.4				
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.				
SOURCE	Rattus norvegicus				
ORGANISM	Rattus norvegicus (Norway rat)				

REFERENCE
AUTHORS

Allen, C., Allen, H., Alsbrooks, S., Andriano, S., Adams, C., Alder, J., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F., Bisswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cessari, H., Cencer, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleaveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Day-Carroll, L., De Aranda, C., Dederich, D., Delgado, O., Denison, S., Detamco, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duvall, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 293183)
Muzny,D.,Marle,M.,Metzker,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,

Allan,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Anguiano,D.,
Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,B.,Baden,H.,
Balwin,D.,Bandaraike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
Biswal,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,
Bryant,N.,Bunay,C.,Burch,P.,Burrell,K.,Calderson,E.,
Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A.,
Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,
Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,
Delgado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Divya,K.,
Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duval,B.,Eaves,K.,
Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,
Fernandez,S.,Finley,M.,Flegg,N.,Forbes,L.,Foster,M.,Foster,P.,
Frazer,C.M.,Gabriel,A.,Ganta,R.,Garcia,A.,Garnier,T.,Garza,M.,
Gebregorgis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,W.,Guevara,W.,
Gunaratne,P.,Haaland,W.,Hamil,C.,Hamilton,C.,Hamilton,K.,
Harvey,Y.,Havlak,P.,Hawes,A.,Henderson,N.,Hernandez,J.,
Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgson,A.,Hogues,M.,
Hollins,B.,Howells,S.,Hulik,S.,Hume,J.,Idlebird,D.,Jackson,A.,
Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,
Karpathy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Kovar,C.,
Kowalski,C.,Kraft,C.L.,Lebow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,
Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,
Lorenshew,L.,Loulsegh,H.,Lozano,R.J.,Lu,X.,Ma,J.,
Maheshwari,M.,Mahindaratne,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,
Mangum,B.,Mapa,P.,Martin,K.,Martin,R.,Martinez,E.,
Manning,S.,McLeod,M.P.,McNeill,T.Z.,Meenan,E.,
Milosavljevic,A.,Miner,G.,Ming,E.,Montemayor,J.,Moore,S.,
Morgan,M.,Morris,K.,Morris,S.,Mundasa,M.,Murphy,M.,Nair,L.,
Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,
Nwaekelemeh,O.,Okwuonu,G.,Olapunbasogun,A.,Pal,S.,Parks,K.,
Pasternak,S.,Paul,H.,Perez,A.,Perez,L.,Pflankoch,C.,
Plopper,F.,Polindexter,A.,Popovic,D.,Primus,E.,Pu,L.-L.,
Puafo,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,
Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richards,S.,Riggs,F.,
Rivas,C.,Rodkey,T.,Rojas,A.,Rose,M.,Rose,R.,Ruiz,S.J.,
Sanders,W.,Savery,G.,Scherer,S.,Scott,G.,Shatsman,S.,Shen,H.,
Shetty,J.,Shvartsbeyn,A.,Sisson,I.,Sitter,C.D.,Smales,D.,
Sneed,A.,Sodergren,E.,Song,X.-Z.,Sorelle,R.,Soosa,J.,
Steinle,M.,Strong,R.,Sutton,A.,Svatek,A.,Tabor,P.,Taylor,C.,
Taylor,T.,Thomas,N.,Thomas,S.,Tingey,A.,Trejos,Z.,Umani,K.,
Valas,R.,Vera,V.,Villaana,D.,Waldron,L.,Walker,B.,Wang,J.,
Wang,Q.,Wang,S.,Warren,J.,Warren,R.,Wei,X.,White,F.,
Williams,G.,Willson,R.,Wlarczyk,R.,Wooden,H.,Wortley,K.,
Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,
Yu,F.,Zhang,J.,Zhou,J.,Zhou,S.,Zhao,S.,Zhou,D.,von
Niederhuesern,A.,Weiss,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
TITLE
JOURNAL
REFERENCE 2 (bases 1 to 293183)
Unpublished
AUTHORS
TITLE
JOURNAL
REFERENCE 3 (bases 1 to 293183)
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
AUTHORS
TITLE
JOURNAL
REFERENCE 4 (bases 1 to 293183)
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GDVC
Center clone name: CH230-10L19

----- Summary Statistics
Assembly program: Phrap; version 0.990329

Consensus quality: 227421 bases at least Q40
Consensus quality: 229231 bases at least Q30
Consensus quality: 230603 bases at least Q20

Estimated insert size: 234846; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 44341: contig of 44341 bp in length
* 44342 44342: gap of unknown length
* 44442 44442: gap of 3901 bp in length
* 48343 48343: gap of unknown length
* 48443 48443: gap of 241035 bp in length
* 289477 289477: gap of unknown length
* 289578 289578: gap of 1849 bp in length
* 291427 291427: gap of unknown length
* 291527 291527: contig of 1657 bp in length.

FEATURES

source

1. 293183

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-10L19"

9810. 10659

/note="clone boundary"

clone_end:17

site:

end_sequence:BH307090"

44442. 46192

/note="wgs_contig"

48443. 51434

/note="wgs contig"

181343. 182203

/note="clone boundary"

clone_end:5p6

site:

end_sequence:BH307132"

misc_feature

misc_feature

misc_feature

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misc_feature

ORIGIN

Query Match 84.7%; Score 43.2; DB 2; Length 293183;
Best Local Similarity 93.8%; Pred. No. 0.11;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RE

LOCUS

ACCESSION

SOURCE

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<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Query March		82.7%	Score 42.2;	DB 2;	Length 189624;
Best Local Similarity		93.6%	Pred NC.0.2;		
Matches	44;	Conservative	0;	Mismatches	3; Indels 0; Gaps 0;
QY	1	GAGGATGACGTCTGAAGAGAGAGAAGAGAGAGAGAGAAQA	47		
Db	78718	GAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAQA	78764		

RESULT 25	AC128202/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	AC128202	189886 bp	DNA					
	Rattus norvegicus clone CH230-423p19, ***	1linear	HTG 20-NOV-2002					
	***, 2 unordered pieces.		SEQUENCING IN PROGRESS					
	AC128202							
	AC128202.3	GI:25139218						
	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.							
	Rattus norvegicus (Norway rat)							
	Rattus norvegicus							

REFERENCE AUTHORS

1 (bases 1 to 18986)

Muzny D Marie, Metzker M Lee, Abramzon S, Adams C, Alder J, Allen C, Allen H, Alsbrooks S, Amin A, Anguiano D, Annaleechech V, Ayogai A, Ayodeji M, Baca E, Baden H, Baldwin D, Bandaranaike D, Barber M, Barsened M, Beahmed F, Bialek K, Blat J, Blankenburg K, Blyth P, Brown M, Bryant N, Bunay C, Burch P, Barrell K, Calderon E, Cardenas V, Carter K, Cavazos I, Caesar H, Center A, Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J, Cleveland C, Cockrell R, Cox C, Coyle M, Gree A, D Souza L, Davila M L, Davis C, Day-Carroll I, De Anna C, Dedrich D, Delgado O, Denison S, Detamo C, Ding Y, Dinh H, Divya K, Diaper H, Duncan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K, Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G, Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Fraser C M, Gabisi A, Gante R, Garcia A, Garner T, Garza M, Gebrgeorgis E, Geier K, Gill R, Grady M, Guerra W, Guetava M, Gunatharatne P, Haaland W, Hamill C, Hamilton C, Hamilton C, Harvey Y, Havlak P, Hawes A, Hladun S L, Hodgson N, Hernandez J, Hollins B, Howell S, Huyls S, Hume J, Idebird D, Jackson A, Jackson L, Jacob L, Jiang H, Johnson B, Johnson R, Jolyvet A, Karpathy S, Kelly S, Kelly S, Khan Z, King L, Kovari C, Kowic C, Kraft C L, Lebow H, Levana J, Lewis L, Li Z, Liu D, Lorensenhuw L, Lu Y, London P, Longacre S, Lopez J, Lorenshuber L, Louisgeed H, Lozado R J, Lu X, Ma J, Manabheri M, Maindardthe M, Mahmoud M, Malloy K, Mangum A, Mangun S, McLeod M P, McNeill T Z, Meenen E, Milosavljevic A, Miner G, Minja E, Montemayor J, Moore S,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Morgan, M., Morris, K., Morris, S., Munidaaa, M., Murphy, M., Natir, L.,
Narkevicius, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwachukwemeh, O., Okunnu, G., Olarnpunagoon, A., Pal, S., Parks, K.,
Pasternack, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Polindexter, A., Popovic, D., Prims, E., Pu, L.,
Puzato, M., Quitzo, J., Rachlin, E., Reeves, K., Reiser, M., Reigh, R.,
Reilly, B., Reilly, M., Renly, E., Reutter, M., Richards, S., Riggs, F.,
Rivers, C., Rodkey, T., Rojag, A., Rose, M., Rose, R., Ruiz, S.,
Sanders, W., Saverly, T., Sojag, A., Sosa, J., Sotale, R., Sosa, J.,
Shetty, J., Shvartsbagn, A., Sisson, I., Silter, C., D., Smaje, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, Q.,
Wang, G., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlezyc, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Weinstock, G., and Weiss, R. A. Smith, D. R., Holt, R. A., Smith, H. O.,
unpublished
2 (bases 1 to 189886)
Morley, K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center

REFERENCE

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 189886)

LIFE
JOURNAL

Submitted (20-NOV-2002) Human Genome Sequencing Consortium,
Direct Submission

COMMENT

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced g1:23908157. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.bsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a contig-scaffold). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center, Paulsen

Center: Baylor College of Medicine
Center code: BCM

Center code: BCM

web site: <http://www.hgsc.bcm.edu>
Contact: hgsc-hellobcm@bcm.edu

Project Information

Center project name: GZMW

center clone name: CH230-423P1

Assembly program: Phrap: version

Consensus quality: 175673 base

consensus quality: 1778888 base

Estimated insert size: 177546:

Quality coverage: 6x in Q20 ba

TE: Estimated insert size max.

(see <http://www.hgsc.bcm.tmc.edu>)

TE: This is a 'working draft' of a

not known and their order in

arbitrary. Gaps between the confi-

ms of N, but the exact sizes of

as record will be updated with
soon as it is available and th

preserved.

* 1 188573: contig of 188573 bp in length
* 188574 188673: gap of unknown length
* 188674 189886: contig of 1213 bp in length.
Location/Qualifiers
source
1. 189886
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-423P19"
1. 1138
/note="wgs_end_extension
clone_end:T7"
complement(4656..4851)
/note="clone_boundary
clone_end:T7
site:
end_sequence:B2183964"
176896..177814
/note="clone_boundary
clone_end:Sp6
site:
end_sequence:B2183966"
180485..182844
/note="wgs_end_extension
clone_end:Sp6"
182895..184020
/note="wgs_end_extension
clone_end:Sp6"
187014..188573
/note="wgs_end_extension
clone_end:Sp6"
ORIGIN
Query Match 82.7%; Score 42.2; DB 2; Length 189886;
Best Local Similarity 93.6%; Pired. No. 0.2;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGAGAGAGAGAGAGAGAGAGAGAGA 47
Db 167288 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 167242
RESULT 26
AL691481 230127 bp DNA linear ROD 26-MAR-2003
LOCUS Mouse DNA sequence from clone RP23-173C3 on chromosome 4 Contains a
DEFINITION muscle enolase 3 beta (Eno3) pseudogene, a mitochondrial H+
transporting ATP synthase F0 complex subunit d (Atp5h) pseudogene
and a CPG island, complete sequence.
AL691481
ACCESSION AL691481.15 GI:22213670
VERSION HTG; Atp5h; CPG island; Eno3.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 230127)
Tracye, A.
Direct Submission
Submitted (17-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hummer@anger.ac.uk Clone requests: clonerequests@anger.ac.uk
On Aug 13, 2002 this sequence version replaced gi:21748253.
----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouse@har.mrc.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormep This sequence
was finished as follows unless otherwise noted: all regions were
either double-stranded or sequenced with an alternate chemistry or
covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at least one
plasmid subclone or more than one M13 subclone; and the assembly
was confirmed by restriction digest, except on the rare occasion of
the clone being a YAC.
RP23-173C3 is from the RPCT-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: PBAC3.6
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
This sequence is the entire insert of clone RP23-173C3 The true
left end of clone RP23-426J14 is at 226462 in this sequence.
Location/Qualifiers
source
1. 230127
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-173C3"
/clone_11b="RPCT-23"
22..695
/note="match: GSS: Em:A2561521"
898..949
/note="26.0 copies 2 mer TG 86% conserved"
complement(956..1118)
/note="B3A repeat: matches 8. 178 of consensus"
1139..1156
/note="4.5 copies 4 mer TTTA 29% conserved"
1183..1193
/note="2.2 copies 5 mer TTATT 22% conserved"
1253..1285
/note="6.6 copies 5 mer TTTTC 34% conserved"
1258..1284
/note="3.0 copies 9 mer CTTTCTTT 38% conserved"
1260..1275
/note="4.0 copies 4 mer TTTC 23% conserved"
1268..1295
/note="28.0 copies 1 mer T 20% conserved"
complement(1344..2435)
/note="11 repeat: matches 3932. 5048 of consensus"
complement(2570..2768)
/note="11 repeat: matches 4623. 4828 of consensus"
2805..2816
/note="2.4 copies 5 mer TACTA 24% conserved"
2956..2970
/note="2.5 copies 6 mer TTTGAT 21% conserved"
4183..4193
/note="2.2 copies 5 mer AGGA 22% conserved"
4943..4989
/note="3.9 copies 12 mer AGAAGAGACG 49% conserved"
4953..4962
/note="5.0 copies 2 mer AG 20% conserved"
4996..5007
/note="2.4 copies 5 mer AATG 24% conserved"
5069..5083
/note="3.0 copies 5 mer ACTGA 21% conserved"
complement(5128..5791)
/note="12 repeat: matches 2228. 2955 of consensus"
6700..6713
/note="2.0 copies 7 mer ATCATTC 28% conserved"

```
repeat_region      complement(14318. .14499)
repeat_region      /note="LI NM repeat: matches 6407. .6587 of consensus"
repeat_region      /note="LI NM repeat: matches 6172. .6380 of consensus"
repeat_region      /note="LI repeat: matches 6172. .6380 of consensus"
misc_feature        complement(15070. .21003)
misc_feature        /note="LI repeat: matches 550. .6618 of consensus"
misc_feature        /note="sequence confirmed by mouse whole genome shotgun
                    Consortium, contig.199864, version 2."
repeat_region      complement(21025. .22191)
misc_feature        /note="LI repeat: matches 59. .591 of consensus"
misc_feature        /note="Cpg island"
misc_feature        /evidence=not_experimental
misc_feature        21755
/note="Tandem repeat. Forced join. Gap size estimated to
be approximately 600bp by restriction digest data."
repeat_region      complement(22209. .23051)
repeat_region      /note="LI repeat: matches 6087. .6933 of consensus"
repeat_region      complement(23252. .23363)
repeat_region      /note="LI repeat: matches 5727. .5846 of consensus"
repeat_region      23414. .23429
repeat_region      /note="16.0 copies 1 mer T 23% conserved"
repeat_region      23522. .23540
```

Query Match	82.7%	Score	42.2;	DB	10;	length	230127;
Best Local Similarity	93.6%						
Matches	44;	Conservative	0.2;				

	Indels	Gaps	
QY	0	0	
I	GAGGATGAAGCTGAAGAGGAGCAACCGAATAATTGGTAAAGTTTGTCGTGTTGTAATCCTCCGATG		

Db

216638 GAGGAGACGAGCAGAGAGAGAGAGA 47
216684

RESULT	27
AC112634	
LOCUS	
DEFINITION	AC112634
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
Rattus norvegicus	
230227 bp DNA linear	
HTG_19-NOV-2002	
WORKING DRAFT SEQUENCE.	
AC112634	
GI_25072799	
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.	
Rattus norvegicus (Norway rat)	

REFERENCES
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AUTHORS

Allen, C., Allen, H., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
Avalos, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,
Baldwin, D., Aoyagi, A., Ayodele, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benamed, F.,
Biswal, K., Blair, J., Blankenhorn, K., Blyth, P., Brown, M.,
Bryant, N., Bunay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederlich, D.,
Delgado, O., Denson, S., Delarmo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falst, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C. M., Gabbili, A., Gatta, R., Garcia, A., Garner, T., Garza, M.,
Geddes, G. E., Geer, K., Gill, R., Grady, M., Guerrero, I., Guzman, P.,
Gunnarsson, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Henderson, R., Hines, S., Hiss, A., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D.,
Jackson, L., Jacob, L., Jiang, H., Johnson, R., Johnson, R., Joliceau, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Krall, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshewna, L., Loulsegod, H., Lozado, R. J., Lu, X., Ma, J.,

TITLE
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Maheshwari, M., Mahindratne, M., Mahmood, M., Malloy, K., Mangun, A., Mangum, B., Mapue, P., Martin, K., Martin, R., Martiny-Bar, E., Maslany, S., McLeod, M.P., McKnight, T.Z., Meenen, E., Milobavskij, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokilemeh, O., Okwuonu, G., Olamundogbon, A., Pal, S., Parke, K., Paternak, S., Paul, H., Perez, A., Perez, J., Pfannkuch, C., Plapper, F., Polndexter, A., Popovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shivaratnam, A., Slison, I., Sitter, C.D., Snajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Swalek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejo, Z., Uemami, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wiczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 230227)
Worley, K.C.
Direct Submission
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 230227)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23365745.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: GSRO
Center clone name: CH230-122c23

Summary Statistics
Assembly program: Phrap; version 0.990129
Consensus quality: 218431 bases at least Q40
Consensus quality: 218953 bases at least Q30
Consensus quality: 220999 bases at least Q20
Baited insert size: 221147; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes

[illegible]

of Molecular and Human Genetics, Baylor Sequencing Center, Department Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:123265853.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hpsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

```

Assembly program: Phrap; version 0.990329
Consensus quality: 218707 bases at least Q40
Consensus quality: 221773 bases at least Q30
Consensus quality: 223342 bases at least Q20
Estimated insert size: 225640; sum-of-confids estimation
Quality coverage: 7x in Q20 bases; sum-of-confids estimation
-----

```

NOTE: Delimited insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is

[illegible]

Query Match	82.7%	Score 42.2;	DB 2;	Length 230313;
Best Local Similarity	93.6%;	Pred. No. 0 2;	Matches 44; Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
Qy	1	GAGSATSAACTGAAAGCGAGCAAGAAGCGAGCAGACGAGGAACA	47	
Dd	160298	GAGCGAAGAGCGAAGAGGAGCAAGAGCGAGCGAGCGAGCGAGCAACA	160344	

RESULT	29
LOCUS	AC111391/c
DEFINITION	Rattus norvegicus clone CH20-14SD10, WORKING DRAFT SEQUENCE, 10
VERSION	AC111391
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE	1 (bases 1 to 268151)
AUTHORS	Muzny, J., McElwain, L., Whitehead, A.P.M., Brown, C., Breen, J., et al.

Aylen, C., Allen, H., Alb Brooks, S., Amin, A., Angulano, D., Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benmahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Birch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Cleveland, C., Cockrell, R., Cox, C., Coyle, R., Chen, Y., Chu, J., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dedertich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C. M., Gabist, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

TITLE	Author
Highly conjugated molecular systems	Wang, W.W.

Journal Unpublished
REFERENCE 2

REFERENCE

**THE
JOURNAL**

REMARK
REFERENCE

JOURNAL

COMMENT FEATURES

Source

CDS

ORIGIN

Query Match	82.4%	Score 42;	DB 4;	Length 1198;
Best Local Similarity	90.0%;	Pred. No. 0.31;		
Matches 45;	Conservative	0;	Mismatch	

[illegible]

Search completed: February 29, 2004, 22:17:19
Job time : 899 secs

RESULT 2

AAD04762

ID AAD04762 standard; DNA; 1353 BP.

XX AAD04762;

XX 04-JUL-2001 (first entry)

XX Human alpha2B-adrenoceptor (alpha2B-AR) gene.

XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction;
XX coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Prinzmetal's variant; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1353

FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT protein"

XX MO200129082-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000MO-F1000913.

XX 22-OCT-1999; 99US-00422985.

XX (JUVN-) JUVANTIA PHARMA LTD OY.

XX Snapir A, Helonen P, Alhopuro P, Karvonen M, Koul M, Pesonen U;
XX Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Myyssönen K;
XX Salonen R, Kaahonen J, Valkonen V,

XX WPI; 2001-300318/31.
XX P-PSDB; AAE00990.

XX New DNA molecule encoding variant specific adrenoceptor protein with
XX deletion of specific amino acids located in the third intracellular loop
XX of the polypeptide, for treating vascular contraction of coronary
XX arteries.

XX Disclosure; Page 27-29; 37pp; English.

XX The present sequence is a gene encoding human alpha2B-adrenoceptor
XX (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
XX (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
XX acids (amino acids 294-311), located in the third intracellular loop of
XX the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
XX Alpha2-AR mediate many of the physiological effects of the
XX catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-
XX adrenoceptor is useful for treating a mammal suffering from vascular
XX contraction of coronary arteries and a disease involving vascular
XX contraction of coronary arteries which is clinically expressed as
XX coronary heart disease (CHD), unstable chronic angina pectoris which is
XX clinically expressed as Prinzmetal's variant form or acute myocardial
XX infarction (AMI). Alpha2B-AR gene is used in gene therapy

XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 100.0%; Score 51; DB 5; Length 1353;

XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 3

AAD4389

ID AAD4389 standard; DNA; 1353 BP.

XX AAD4389;

XX 13-DEC-2002 (first entry)

XX Human alpha-2B-adrenoceptor gene.

XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
XX hypertension; hypotensive; gene; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1353

FT /tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"

XX MO200266617-A1.

XX 29-AUG-2002.

XX 13-FEB-2002; 2002MO-F1000113.

XX 20-FEB-2001; 2001FI-00000323.

XX (JURI-) JURILAB LTD OY.

XX Salonen J;

XX WPI; 2002-667063/71.

XX P-PSDB; AAE2634.

XX Determining a risk of hypertension and targeting treatment in a subject by
XX determining the pattern of alleles encoding a variant alpha-2-
XX adrenoceptor.

XX Disclosure; Page 27-29; 35pp; English.

XX The invention relates to a method for detecting a risk of hypertension by
XX determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing the
XX antihypertensive effect of compounds. The present sequence is human alpha
XX -2B-adrenoceptor gene

XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 100.0%; Score 51; DB 6; Length 1353;

XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 4

AAQ14151

ID AAQ14151 standard; DNA; 2064 BP.

XX AAQ14151;

XX 06-JAN-1992 (first entry)

XX Human alpha 2 beta adrenergic receptor gene.

XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.

XX Homo sapiens.

CC of target polynucleotide. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 7; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 1292 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342
RESULT 7
ABZ42624
ID ABZ42624 standard; DNA; 3274 BP.
XX
AC ABZ42624;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related disease; cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; de.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
P-PsDB; ABP81780.
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42623 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 7; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930
RESULT 8
AAS68926
ID AAS68926 standard; cDNA; 291 BP.
XX
AC AAS68926;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #4730.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
P-PsDB; ABG04739.
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnosis, forensics, gene mapping, identification of mutations

QY 1 GAGGATGAAGCTGAAGAGGAGAAGAGGAGGAGGAGGAGAGAG 48

XX Bax; Bax-resistance; cytosolic; fungicide; immunosuppressive; virucide;
KM vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KM apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KM neurodegeneration; cell death; ss.
XX Saccharomycetes cerevisiae.
XX MO200264766-A2.
XX 22-AUG-2002.
XX 21-DEC-2001; 2001WO-EP015398.
XX 22-DEC-2000; 2000EP-00870318.
XX 04-JAN-2001; 2001EP-00870002.
XX 09-JAN-2001; 2001EP-00870003.
XX (JANC) JANSSEN PHARM NV.
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX WPI; 2002-667002/71.
XX P-PSDB; ABG93152.
XX
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medication for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX
XX Claim 36; Fig 1; 344pp; English.
XX
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytosolic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention.
XX
XX Sequence 1721 BP; 501 A; 400 C; 341 G; 479 T; 0 U; 0 Other;
SQ
XX
XX Query Match 79.6%; Score 40.6; DB 6; Length 1721;
XX Best Local Similarity 91.5%; Pred. No. 0.2;
XX Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
DB 631 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 585

RESULT 16

AAD55832
ID AAD55832 strand; cDNA; 2663 BP.
XX
AC AAD55832;
XX
XX 07-AUG-2003 (first entry)
XX
DE Human nucleic acid associated protein (NAAP)-3 cDNA.

XX Human; nucleic acid associated protein; NAAP; stroke; AIDS; neurotic;
KM cancer; atherosclerosis; neurological; epilepsy; Huntington's disease;
KM developmental disorder; antiinflammatory; neuroprotective; thymimetic;
KM Cushing's syndrome; infection; gene therapy; cytosolic; anticonvulsant;
KM cerebroprotective; hypothyroidism; cell proliferative disorder; allergy;
KM gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 237..2444
XX /*tag= a
XX /product= "Human NAAP protein"
XX
XX MO2003006618-A2.
XX
XX 23-JAN-2003.
XX
XX 10-JUL-2002; 2002WO-US021971.
XX
XX 12-JUL-2001; 2001US-0305089P.
XX 12-JUL-2001; 2001US-0305104P.
XX 13-JUL-2001; 2001US-0305125P.
XX 13-JUL-2001; 2001US-0305190P.
XX 19-JUL-2001; 2001US-0306960P.
XX 20-JUL-2001; 2001US-0306994P.
XX 27-JUL-2001; 2001US-0308170P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Swarnakar A, Richardson TW, Warren BA, Griffin JA, Tang YT;
PI Yde H, Baughn MR, Emerling BM, Lal PG, Lu DM, Forsythe IU;
PI Ramkumar J, Li JX, Becha SD, Duggan BM, Sanjanwala MM, Lee EA;
PI Burford N, Elliott VS, Ison CH, Ding L, Borowsky ML, Yao MG;
PI Barroso I, Tran B, Walla NK, Hafalia AJA, Nguyen DB, Lu Y;
PI Arvizu CS;
XX
XX WPI; 2003-221732/21.
XX P-PSDB; AAE37016.
XX
XX New human nucleic acid associated proteins (NAAP), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
PT infections.
XX
XX Claim 5; Page 232; 260pp; English.
XX
XX The invention relates to human nucleic acid associated proteins (NAAP)
CC and their corresponding nucleic acid sequences. The invention is useful
CC in diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of NAAP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. It is also useful in assessing the effects of
CC exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of NAAP. The NAAP or its fragments are useful in screening
CC compounds for which acts as their agonist or antagonist. The microarray
CC is useful in monitoring or measuring protein-protein interactions, drug-
CC target interactions, and gene expression profiles. NAAP DNA is used in
CC gene therapy. The present sequence is human NAAP cDNA
XX
XX Sequence 2663 BP; 875 A; 497 C; 715 G; 576 T; 0 U; 0 Other;
SQ
XX
XX Query Match 79.6%; Score 40.6; DB 7; Length 2663;
XX Best Local Similarity 91.5%; Pred. No. 0.21;
XX Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
DB 930 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 976

XX	Murine; mouse; gene trap technology; gene trapped sequence; GTS;
KW	gene identification, functional genomic analysis; gene discovery;
KW	gene expression analysis; cross species hybridisation analysis;
KW	antisense inhibition; gene targeting; gene; ss.
XX	
OS	Mus sp.
XX	
XX	US2002161207-A1.
PN	
PD	31-OCT-2002.
XX	
PF	30-NOV-2000; 2000US-00728444.
XX	
PR	01-DEC-1999; 99US-0168360P.
XX	
PA	(FRIE/) FRIEDRICH G.
XX	(ZAMB/) ZAMBROWICZ B.
PA	(SAND/) SANDS A T.
XX	
P1	Friedrich G, Zambrowicz B, Sands AT;
XX	
DR	WPI; 2003-288124/28.
XX	
PT	New murine polynucleotides comprising gene trapped sequences, useful in
PT	functional genomic analysis, in the development of new therapeutic or
PT	diagnostic agents, for diagnostic gene expression analysis or for genetic
PT	manipulations.
XX	
PS	Claim 2; SEQ ID NO 146; 29pp; English.
XX	
CC	The present invention relates to novel murine cDNAs produced using gene
CC	trap technology. The OMNIBANK gene trapped sequences (GTSs) are
CC	individually identified novel genes, and are useful in functional genomic
CC	analysis, in the discovery and development of new therapeutic and
CC	diagnostic agents, for gene discovery, for diagnostic gene expression
CC	analysis, for cross species hybridisation analysis, and for genetic
CC	manipulations such as antisense inhibition or gene targeting. The
CC	polynucleotides of the invention are also useful for isolating cDNAs,
CC	genomic clones or full-length genes/polynucleotides, or their homologues,
CC	heterologues, paralogues or orthologues, that are capable of hybridising
CC	to one or more of the new murine polynucleotide sequences. The
CC	polynucleotides are also useful for identifying the coding regions of the
CC	murine genome, and as hybridisation probes. ABX90657-ABX91862 represent
CC	the murine GTSs of the invention. Note: The sequence data for this patent
CC	did not form part of the printed specification, but was obtained in
CC	electronic format directly from the USPTO web site at
CC	seqdata.uspto.gov/patseqidentry.html
XX	
SO	Sequence 223 BP; 64 A; 31 C; 65 G; 48 T; 0 U; 15 Other;
XX	
Query Match	78.4%; Score 40; DB 7; Length 223;
Best Local Similarity	89.6%; Pred No. 0.28;
Matches	43; Conservative 0; Mismatches 5; Indels 0; Gaps 0
QY	1 GAGGATGAAGCTGAAGAGGAGGAAGGAGGAGGAGGAGGAAG 48
DB	14 GAGGAGGAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
XX	
RESULT 20	
XX	AA875432
XX	AA875432 standard; cDNA; 224 BP.
AC	
XX	AA875432;
XX	
XX	13-FEB-2002 (first entry)
DE	DNA encoding novel human diagnostic protein #11236.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX	

XX	Homo sapiens.
XS	WO200175067-A2.
PN	11-OCT-2001.
PD	
XX	30-MAR-2001; 2001WO-US008631.
PF	
XX	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.
XX	(HYSE-) HXSEQ INC.
PA	
XX	Dmanac RT, Liu C, Tang YT;
PI	
DR	WPI; 2001-639362/73.
DR	P-PSTDB; ABG11245.
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity.
PS	Claim 1; SEQ ID NO 11236; 103pp; English.
XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC	sequences. (I) is useful as hybridisation probes, polymerase chain
CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC	and in recombinant production of (II). The polynucleotides are also used
CC	in diagnostics as expressed sequence tags for identifying expressed
CC	genes. (I) is useful in gene therapy techniques to restore normal
CC	activity of (II) or to treat disease states involving (II). (II) is
CC	useful for generating antibodies against it, detecting or quantitating a
CC	polypeptide in tissue, assessing molecular weight markers and as a food
CC	supplement. (II) and its binding partners are useful in medical imaging
CC	of sites expressing (II). (I) and (II) are useful for treating disorders
CC	Involving aberrant protein expression or biological activity. The
CC	polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC	coding sequences of the invention. Note: The sequence data for this
CC	patent do not appear in the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 224 BP; 117 A; 9 C; 89 G; 9 T; 0 U; 0 Other;
Query Match	78.4%; Score 40; DB 5; Length 224;
Best Local Similarity	89.6%; Pred. No. 0.29;
Matches 43; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
OY	1 GAGATGAAGCTGTAAGAAGAGAAAGACGAGCAGCGAAGCAAGAG 48
Db	49 GAAGAAGAAAGAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAG 96
RESULT 21	
ABQ98152/c	
ID	ABQ98152 standard; CDNA; 234 BP.
XX	ABQ98152;
AC	
XX	
DT	30-OCT-2002 (first entry)
DE	Mouse ES cell related cDNA SEQ ID NO 1420.
XX	
KW	Mouse; ES cell; gene trapped sequence; GT5; gene expression;
KW	development disorder; cell differentiation disorder; gene; ss.
XX	Mus bp.
OS	
XX	

[illegible]

RESULT 28	
ABR65237	
ID	ABR65237 standard; cDNA, 2663 BP.
XX	
AC	ABR65237;
XX	
DT	02-JUL-2002 (first entry)
XX	
DE	Arabidopsis cDNA encoding a transcription factor #89.
XX	
KW	Plant; ss; gene; transcription factor; transgenic; agriculture;
KW	metabolic chemical; environmental stress; drought;
KW	microbial disease resistance; herbicide resistance; seed yield;
KW	fruit yield; growth rate; leaf senescence; flower senescence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	WO200215675-A1.
XX	
PD	
XX	
26-FEB-2002.	
XX	
PF	
XX	
22-AUG-2001; 2001WO-US026189.	
PR	
22-AUG-2000; 2000US-0227439P.	
PR	
16-NOV-2000; 2000US-00713994.	
XX	
18-APR-2001; 2001US-00837944.	
XX	
PA	(MEND-) MENDEL BIOTECHNOLOGY INC.
PA	(PTLG/) PILGRIM M.
PA	(GREE/) CREELMAN R.
PA	(DOBE) DUBELL A J.
PA	(HEAR/) HEARD J.
PA	(CIAN) CIANG C.
PA	(KEDD/) KEDDIE J.

[illegible]

PD 06-MAR-2003.
PF 22-MAR-2000; 2000US-00533029.
PR 22-MAR-2000; 2000US-00533029.
XX
PA (HEAR/) HEARD J.
PA (BROU/) BROUN P.
PA (RIEC/) RIECHMANN J L.
PA (KEDD/) KEDDIE J.
PA (PINE/) PINEDA O.
PA (ADAM/) ADAM L.
PA (SAMA/) SAMAH A R.
PA (ZHAN/) ZHANG J.
PA (YUGJ/) YU G.
PA (RATC/) RATCLIFFE O.
PA (PIIG/) PILGRIM M.
PA (JIANG/) JIANG C.
PA (REUB/) REUBER L.
XX
XX Heard J., Broun P., Riechmann JL, Keddie J., Pineda O., Adam L,
PI Samaha R., Zhang J., Yu G., Ratcliffe O., Pilgrim M., Jiang C., Reuber L,
DR P-PSDB; AB043116.
XX MPI: 2003-521768/49.
XX
XX New transgenic plants comprising a recombinant gene that alters the
PT plant's disease tolerance or resistance, useful in plant breeding, e.g.
PT for generating plants with improved tolerance or resistance to diseases,
PT pests or pathogens.
XX
XX Claim 14; Page 45-46; 124pp; English.

The invention relates to a transgenic plant, comprising a recombinant polynucleotide that alters the plant's disease tolerance or resistance when compared with the same trait of another plant lacking the recombinant polynucleotide. The recombinant polynucleotide comprises a nucleotide sequence, which encodes a polypeptide comprising at least 6 consecutive amino acids of any of 56 transcription factor proteins appearing as AB043093-AB043148. Also included are altering the disease tolerance or resistance of a plant by: (a) transforming a plant with the recombinant polynucleotide; (b) selecting the transformed plants; and (c) identifying a transformed plant with an altered disease tolerance or resistance), altering the expression levels of at least one gene in a plant by transforming the plant with the recombinant polynucleotide, altering a plant's trait (comprising: (a) providing a database sequence; (b) comparing the database sequence with the polypeptide or polynucleotide cited above; (c) selecting a database sequence that meets the selected sequence criteria; and (d) transforming the selected database sequence in the plant); and altering a plant's trait (comprising: (a) providing a test polynucleotide; (b) hybridising the test polynucleotide at low stringency with the recombinant polynucleotide cited above; and (c) transforming the hybridising test polynucleotide in a plant to alter a trait of the plant. The transgenic plant is useful in plant breeding, particularly for generating plants with improved tolerance or resistance to diseases. The plants have commercial utility for increasing tolerance or resistance to pathogens and pests. The present sequence is an Arabidopsis thaliana transcription factor cDNA of the invention

Sequence 2663 BP; 836 A; 544 C; 625 G; 658 T; 0 U; 0 Other;
XX
XX

Query Match 78.4%; Score 40; DB 8; Length 2663;
Best Local Similarity 89.6%; Pred No. 0.29;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0

1 GAGGTGAAGCTGTAAGAGAGAGAAGAGAAGAGAAGAGAAGAGAAG 48
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 865 GATGACGAAGATGAGAGAGAGAAGAGAAGAGAAGAGAAGAGAAG 912

RESULT 30
ADD30227

RESULT 8
AZ288043/c
LOCUS
DEFINITION RPCI-23-102K10.TV RPCI-23 Mus musculus genomic clone
ACCESSION RPCI-23-102K10, genomic survey sequence.
VERSION A2288043
KEYWORDS A2288043.1 GI:9529829
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 713)
REFERENCE
AUTHORS Zhao, S., Niernan, W., Feldblum, T., Malek, J., Shatsman, S., de
Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
OTHER GSSs: RPCI-23-102K10.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@tigr.org, med.bu@falo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bu@falo.edu/orderingframe.htm>)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 102 row: K column: 10
Seq primer: T7
Classes: BAC ends.
FEATURES
Location/Qualifiers
1..713
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-102K10"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcORI; Site_2: EcORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcORI and EcORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match 81.6%; Score 41.6; DB 28; Length 713;
Best Local Similarity 91.7%; Pred. No. 46;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAG 48
|||||
DB 101 GAGGAGGAAGAGAGGAGAGGAGGAAGAGGAGAGGAGAGGAGAGAG 54
|||||
RESULT 9
B1067787
LOCUS
DEFINITION B1067787 640 bp mRNA linear EST 15-JUN-2001
cdna.pK007.124 normalized chicken fat cDNA library Gallus gallus
pK007.124 5' similar to gi|4506411
ref|NP_002874.1| Ran GTPase activating protein 1; Fugu (Homo
sapiens) gi|11418178 ref|XP_010014.1| Ran GTPase activating protein
1 (Homo sapiens) sp|P46060|RGPI HUMAN RAN-GTPASE ACTIVATING PROTEIN
1 pfr|118146 RANGAPI - human pfr|JC, mRNA sequence.
ACCESSION B1067787

VERSION B1067787.1 GI:14475309
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 640)
REFERENCE
AUTHORS Cogburn, L.A., Morgan, R.W., and Burnside, J.
Chicken ESTs from fat
Unpublished (2001)
TITLE
JOURNAL
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES
source
Location/Qualifiers
1..640
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/cd_xref="pK007.124"
/clone="pK007.124"
/sex="Male and Female"
/issue_type="fat"
/lab_host="E.coli EMDH108"
/clone_lib="normalized chicken fat cDNA library"
/note="Vector: pSPORT1"
ORIGIN
Query Match 79.6%; Score 40.6; DB 12; Length 640;
Best Local Similarity 91.5%; Pred. No. 71;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAGA 47
|||||
DB 180 GAGGAGGAAGATGAAGAGGAGGAAGAGGAGAGGAGAGGAGAGAGA 226
|||||
RESULT 10
BH309086/c
LOCUS
DEFINITION BH309086 668 bp DNA linear GSS 03-DEC-2001
CH230-4116.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-4116, genomic survey sequence.
ACCESSION BH309086
VERSION BH309086.1 GI:17234555
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 668)
REFERENCE
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P., and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcORI segment
Unpublished (1999)
TITLE
JOURNAL
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 4 row: L column: 16
Seq primer: T7

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mtb-3xHA/lacZ insertion.
Seg primer: GGCTCTCTTCTTGGAGTAC
Class: transposon-tagged.

FEATURES
source

1.797
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="Y2278 - S288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
/lab_host="E. coli"
/clone_lib="mtb-3xHA/lacZ insertion library, strain Y2278"
/note="Vector: pHS6-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mtb-3xHA/lacZ multitransposon containing lacZ, URA3, and tetr resistance."

ORIGIN

Query Match 79.6%; Score 40.6; DB 28; Length 797;
Best Local Similarity 91.5%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAACTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
DB 260 GAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 306

RESULT 14
LOCUS B2227940/c 826 bp DNA linear GSS 12-OCT-2002
DEFINITION CH230-400D22.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION B2227940
VERSION B2227940.1 GI:23886481
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 826)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Zhao, S., Shetty, J., Shateman, S., Teegase, G., Geer, K.,
Shvartsbeyn, A., Gebregiorgis, E., Overton, L., Russell, D., Chen, D.,
Ritger, P., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230

FEATURES
source

(http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ordering information.html). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 400 row: D column: 22
Seg primer: SP6
Class: BAC ends.
Location/Qualifiers
1.826
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SENhsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-400D22"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; CHORI-230 Rat (BN/SENhsd/MCW) BAC library produced by Pieter de Jong"

ORIGIN

Query Match 79.6%; Score 40.6; DB 28; Length 826;
Best Local Similarity 91.5%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAACTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
DB 794 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 748

RESULT 15
LOCUS BQ231724 873 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT 7560029 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055864
5' mRNA sequence.
ACCESSION BQ231724
VERSION BQ231724.1 GI:20413124
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC/DCPD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1316 row: m column: 17
High quality sequence scop: 703.
Location/Qualifiers
1.873

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6055864"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: Skin; Vector: pCMV-SORT2; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

D_b

103 GACGAGGAAGAGAGAGAGAAGAGAGAGAGAGAGAGA 47
149

RESULT 16
BM807097

DEFINITION	AGENCOURT_6552940 NIH_MGC_85 Homo sapiens cdna clone IMAGE:5552038
ACCESSION	BM807097
	5', mRNA sequence.

KEYWORDS	EST.	GI:19123920
KEYWORDS	EST.	GI:19123920
SOURCE	Homo sapiens (human)	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1362) . rna;cat; catarrhini; hominidae; homo.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished. (1999)
Contact: Robert Strausberg ph D

Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.jnl.gov>

FEATURES	Location/Qualifiers
source	1. .1362

ORIGIN

Query Match	79.6%	Score 40.6;	DB 12;	Length 1362;
Best Local Similarity	91.5%;	Pred. No. 78;		
Matches 43;	Conservative 0;	Mismatches 4		

D

QY Db	 The diagram shows two horizontal lines representing DNA sequences. The top line is labeled 'QY' and the bottom line is labeled 'Db'. Vertical tick marks indicate positions where the sequences are aligned or compared. There are several vertical bars of varying lengths connecting the two lines, indicating regions of similarity or specific mutations. Some bars are solid, while others have gaps or different patterns.	I GAGGATGAAGCTGAAGAGCGAAGAGGAGGAGGAGGAGAGA 47 47 GAGGAGAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 93
----------	--	--

RESULT 17
BB852469

DEFINITION	BB852469	453 bp	RNA	linear	EST 26-NOV-2001
	cDNA clone G370007K15 5', mRNA sequence.				
ACCESSION	BB852469				
	Mus musculus				

KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

metazoa; chordata; Craniata; Vertebrata; Euteleostomi.

[illegible]

TITLE	RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al 2001)
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
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89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

Unpublished (2001)
Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suheiho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
E-mail: gsc@riken.go.jp

E-mail: genome-tee@cc.riken.go.jp,
 URL: <http://genome.sgc.riken.go.jp/>
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujikake, S., Inoue, K., Togawa, I., Iwama, M., Ohara, E.,
 Matsubara, S., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsushima, S., Kawai, T., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.

AKASH Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res*
10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugihara, Y. and Hayashizaki, Y.

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computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001). Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES	Location/Qualifiers
source	1. .453

ORIGIN

Query Match	79.2%;	Score 40.4;	DB 10;	Length 453;
Best Local Similarity	88.0%;	Pred. No. 74;		
Matches 44;	Conservative 0;	Mismatches 6;		

Qy
1 GAGGATGAAGCTGAAGAAGAGAAAGAGAGAGAGAGAGAAAGTGG 50
|||
75 GAGGAGTGG 124

Dd

RESULT 18
BX519271

DEFINITION	Accession
BX519271 Sngano mouse kidney mRna Mus musculus cdna clone IMAGE:980J204714 ; IMAGE:1922035, mRNA sequence.	EST 27-JUN-2003
BX519271	

KEYWORDS	EST.	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 553) Mamalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Mouse Unigeneset - RZPD2 Unpublished (2003)

Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGp98J204714.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Mouse Unigeneset - RZPD2 (RZPDLIB No. 981) http://www.rzpd.de/clonecards/cgi-bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 101 Fax: +49 30 32639 111

www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: 5'ugf, primer sequence: CTCTGCTCTTAAGCTCGG.

FEATURES SOURCE location/Qualifiers

1..553

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL"

/db_xref="taxon:10090"

/clone="IMAGp98J204714 ; IMAGE:1922035"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Sugano mouse kidney mklia"

/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII (CACCATGG); Site 2: DraIII (CACCATGG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTCGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCATGG, 3' site CACCATGG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' and primer CTCTGCTCTTAAGCTCGG and 3' end primer CGACTCGACTCGACACA."

ORIGIN

Query Match 79.2%; Score 40.4; DB 13; Length 553; Best Local Similarity 88.0%; Pred. No. 76; Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Dy 1 GAGCGTGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGG 50
|||||
1 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGG 97

RESULT 19
LOCUS A2208950 786 bp DNA linear GSS 31-AUG-2000
DEFINITION SP.0138_A2.C06.T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=138 Col=12 Row=E, genomic survey sequence.
ACCESSION A2208950
VERSION A2208950.1 GI:8422136
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 786)

AUTHORS

Cameron,R.A., Mahairas,G.,Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ertenson,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.

TITLE

A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

MEDLINE

20402566

PUBMED

10920195

COMMENT

Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 138 row: E column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 786.
Location/Qualifiers
1..786
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone_plate=138 Col=12 Row=E"
/clone_id="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACet.6; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 79.2%; Score 40.4; DB 28; Length 786;
Best Local Similarity 88.0%; Pred. No. 80;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Dn

94 GAGATGTAAGGAGGAGGAAGAAGAGAGAGAGAGAGAGAGTG 50
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1 GAGCATGAAGCTGAAGCAGCAAGAAAGAGAGAGAGAGAGAGTGTG 50
|||||

Oy

BZ152227 799 bp DNA linear GSS 11-OCT-2002
CH230-504N18.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-504N18, genomic survey sequence.
BZ152227
BZ152227.1 GI:23793178
GSS.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurignathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 799)
Zhao,S., Shetty,J., Shateman,S., Tsegaye,G., Geer,K.,
Shvartsbeym,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-504N18.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdjong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ordering information.htm). BAC end

RESULT 20

BZ152227
LOCUS 1
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

submicrogram amounts of total RNAs by a universal PCR amplification method
Genome Res. 11 (9), 1553-1558 (2001)
21429098
11544199
COMMENT
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@jhsun.grc.nia.nih.gov
Phone: A0231 row: H column: 07
Seq primer: M13 Reverse
High quality sequence stop: 330
POLYA=No.

FEATURES
SOURCE

1. 330
/organism="Mus musculus"
/mol_type="mRNA"
/strains="C57BL6"
/db_xref="tasest:A0231H07-5"
/db_xref="taxon:10090"
/clone="NIA:A0231H07 IMAGE:30731418"
/sex="male"
/dev_stage="embryonic day 8"
/lab_host="PH108"
/clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library (long-subtracted)"
/notes="vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://jgsun.grc.nia.nih.gov/cDNA>) This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544191]. EG cells were obtained from Dr. Brigida L.M. Hogan and RNA was prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells were cultured at 37° C, 5% CO2 in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 2 mM glutamine, penicillin/streptomycin, and sodium pyruvate, 0.1 mM beta-mercaptoethanol, 1 mM units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen: 5'-GACTAGTCTGATCGGACGCGCCCTCTTTTCTTTT-3') purified by ethanol-precipitation. The cDNAs were ligated to lome-linker IL-Sal4, purified by phenol/chloroform, and cDNAs were amplified by long-range high fidelity PCR using Ex-Taq polymerase (Takara) with a primer Sal4-5. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr Kazuhiro Kondo at AISTN Cosmos. Then the subtracted cDNAs were cloned into AISTN Cosmo. Then the pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo."

ORIGIN

[illegible]

RESULT 26	AL135731	331 bp	mRNA	linear	EST 04-SEP-2003
LOCUS	AL135731				
DEFINITION	DKFZ433H0531_r1 434 (synonym: hres3) Homo sapiens cDNA clone				

Accession	DKFZp434H0531.5', mRNA sequence
Version	AL135731
Keywords	AL135731.1 GI:6603918
Source	EST.
Organism	Homo sapiens (human)
	Homo sapiens

REFERENCE	Blum, H., Bauererachs, S., Mewes, W., Weill, B. and Wiemann, S., 1 (bases 1 to 331)
AUTHORS	Blum, H., Bauererachs, S., Mewes, W., Weill, B. and Wiemann, S.
TITLE	EST (Blum, H., Bauererachs, S., Mewes, H.W., Weill, B. and Wiemann, S.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS

JOURNAL
COMMENT

MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis,
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by LMU (Ludwig Maximilians University,
 Munich/Germany) within the cDNA sequencing consortium of the German
 Genome Project.
 No st sequence available.
 This clone (DKFZp434H0531) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
 Location/Qualifiers
 1..311

FEATURES

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/2genus="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="DKFZ434H0531"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="434 (synonym: htees3)"
/note="Vector: pSPori1; Site 1: Not."
ORIGIN

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ORIGIN

Query Match	78.4%	Score 40;	DB 9;	Length 331;
Best Local Similarity	89.6%	Pred. No. 86;		
Matches 43;	Conservative 0;	Mismatches		

[illegible]

RESULT	27
CD564037/c	
LOCUS	
DEFINITION	
CD564037	358 bp mRNA
B0473A03-5	NIA Mouse E6.5 whole embryo cDNA library (long) Mus EST 11-JUN-2003
musculus	cDNA clone NIA:B0473A03 IMAGE:3045634 5' mRNA sequence.
ACCESSION	CD564037
VERSION	GI:31607930
KEYWORDS	
SOURCE	Mus musculus (house mouse)

ORGANISM

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 358)
TITLE	Piao, Y., Ko, N.-T., Lim, M.-K. and Ko, M.-S. H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
JOURNAL	Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE	21429098
PubMed	11544199
COMMENT	Contact: Dawood B. Piao, jk@genomics.org

Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@isun.gic.nia.nih.gov
Plate: B0473 row: A column: 03


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/lab host="DH10B"  
/clone.lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library  
(long)"  
/notes="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
extracted from a pool of four embryos at 7.5-days  
postcoitum. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer [Invitrogen:  
5'-pGACTAGTCTAGATCGCGAGCGCCCTTTT-3'] from  
7 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker L1-SalI, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.2 kb. The library was constructed  
by Yulan Piao (NIA)."
```

ORIGIN

```
Query Match      78.4%; Score 40; DB 14; Length 373;  
Best Local Similarity 89.6%; Pred. No. 87;  
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      1 GAGGATGAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 48  
        ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB      270 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 223
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Search completed: February 29, 2004, 21:48:03  
Job time : 2176 secs
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; Patent No. 6287762
; GENERAL INFORMATION:
; APPLICANT: CROUZET, Joel
; APPLICANT: SCHERMAN, Daniel
; APPLICANT: WILS, Pierre
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
; TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mallescop 3C43
; CITY: Collegenville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,038
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/15162
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/01468
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST94090-US
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; US-08-860-038-16

Query Match 72.2%; Score 36.8; DB 3; Length 58;
Best Local Similarity 85.4%; Pred. No. 0.099;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 56 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9

RESULT 11
US-09-580-923-15
; Sequence 15, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wils, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
; TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
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; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; PRIOR FILING DATE: 1995-11-08
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; TYPE: DNA
; LENGTH: 58
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; US-09-580-923-15

Query Match 72.2%; Score 36.8; DB 4; Length 58;
Best Local Similarity 85.4%; Pred. No. 0.099;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 7 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 54

RESULT 12
US-09-580-923-16/c
; Sequence 16, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
; APPLICANT: Crouzet, Joel
; APPLICANT: Scherman, Daniel
; APPLICANT: Wils, Pierre
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
; TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
; FILE REFERENCE: 03804.0138-01
; CURRENT APPLICATION NUMBER: US/09/580,923
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 08/860,038
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/FR95/01468
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; US-09-580-923-16

Query Match 72.2%; Score 36.8; DB 4; Length 58;
Best Local Similarity 85.4%; Pred. No. 0.099;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 56 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9

RESULT 13
US-09-894-998A-34/c
; Sequence 34, Application US/09894998A
; Patent No. 6537555
; GENERAL INFORMATION:
; APPLICANT: Hosken, Nancy Ann
; APPLICANT: Craig H. Day
; APPLICANT: Davin C. Dillon
; APPLICANT: McGowan, Patrick
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
```


RESULT 3

US-10-001-073-1
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Ligggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1

Query Match 100.0%; Score 51; DB 14; Length 1353;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGT 51
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DB 880 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 930

RESULT 4

US-10-305-720-1181
; Sequence 1181, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1181
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

Query Match 100.0%; Score 51; DB 15; Length 2072;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGT 51
|||||

DB 1292 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGT 1342

RESULT 5

US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 100.0%; Score 51; DB 14; Length 3274;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGT 51
|||||

DB 880 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 930

RESULT 6

US-10-034-650-31/c
; Sequence 31, Application US/10034650
; Publication No. US20030216558A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000128
; CURRENT APPLICATION NUMBER: US/10/034,650
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/474,377
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Paetsrq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 68233
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-034-650-31

Query Match 81.6%; Score 41.6; DB 15; Length 68233;
Best Local Similarity 91.7%; Pred. No. 0.0037;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 48
|||||

DB 66088 GAGAGGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 66041

RESULT 7

US-09-972-546-16/c
; Sequence 16, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMAYER, STEPHEN M.
; APPLICANT: CATE, RICHARD L.
; APPLICANT: SAH, DINAH M.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116US
; CURRENT APPLICATION NUMBER: US/09/972,546
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 215980
; TYPE: DNA

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/ ORGANISM: Mus sp.
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (1001)..(1100)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (2123)..(2222)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (3728)..(3827)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (5168)..(5267)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (7481)..(7580)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (8849)..(8948)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (10375)..(10474)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (12270)..(12369)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (13438)..(13537)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (15902)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (15939)..(16038)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (18223)..(18322)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
/ LOCATION: (20974)..(21073)
/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
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/ OTHER INFORMATION: a, t, c, g, other or unknown
/ NAME/KEY: modified_base
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APPLICANT: Heimonen, Paula
 APPLICANT: Alhopenro, Pia
 APPLICANT: Karvonen, Matti
 APPLICANT: Koulun, Markku
 APPLICANT: Pesonen, Ullamari
 APPLICANT: Scheinin, Mika
 APPLICANT: Salonen, Jukka T
 APPLICANT: Tuomala, Tomi-Pekka
 APPLICANT: Lakka, Timo A
 APPLICANT: Nyssanen, Kristina
 APPLICANT: Salonen, Raita
 APPLICANT: Kauppinen, Jussi
 APPLICANT: Valkonen, Veli-Pekka
 TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
 TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
 FILE REFERENCE: Alpha-2B-AR variant
 CURRENT APPLICATION NUMBER: US/09/825,923
 CURRENT FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 09/422,985
 PRIOR FILING DATE: 2000-05-25

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RESULT 10
US-09-728-444-146
; Sequence 146 Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020161207A1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Murant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0100-USA
; CURRENT APPLICATION NUMBER: US/09/728,444
; PRIOR APPLICATION NUMBER: 2000-11-30
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1206
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146

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RESULT 11
US-09-728-446-1420/c
; Sequence 1420, Application US/09728446
; Patent No. US20020081668A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020081668A1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0101-USA
; CURRENT APPLICATION NUMBER: US/09/728,446
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,270
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ. ID NOS: 1461
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ. ID NO 1420
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(234)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-446-1420

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Query Match          78.4%; Score 40; DB 9; Length 234;
Best Local Similarity 89.6%; Pred. No. 0.013;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps
QY      1 GAGGATGAGCTGTAAGAGGAGGAAAGGAGAGGAGGAGGAGAGAG 48
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Db      174 GAGGAGGAGAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGAG 127
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RESULT 12
US-09-728-444-124
; Sequence 124, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020161207A1 Murine Polynucleotide Sequences
; FILE REFERENCE: LEX-0100-USA and Mutant Cells and Mutant Animals Defined Thereby
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US/09/728,444
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1206
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 330

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? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1) ...(330)
? OTHER INFORMATION: n = A,T,C or G
US-09-728-444-124

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Query, Match	78.4%;	Score 40;	DB 9;	Length 330;
Best Local Similarity	89.6%;	Pred. No. 0.013;		
Matches	43;	Conservative	0.013;	Microbial

[illegible]

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      RESULT 13
      US-10-425-114-10213
      ; Sequence 10213. Application US/10425114
      ; Publication No. US2004003488A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Liu, Jingdong
      ; APPLICANT: Zhou, Yihua
      ; APPLICANT: Kovalic, David K.
      ; APPLICANT: Screen, Steven E.
      ; APPLICANT: Tabaska, Jack E
      ; APPLICANT: Cao, Yongwei
      ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
      ; FILE REFERENCE: 38-21(53313) B
      ; CURRENT APPLICATION NUMBER: US/10/425,114
      ; CURRENT FILING DATE: 2003-04-28
      ; NUMBER OF SEQ. ID NOS.: 73128
      ; SEQ. ID NO 10213
      ; LENGTH: 642
      ; TYPE: DNA
      ; ORGANISM: Glycine max
      ; FEATURE:
      ; OTHER INFORMATION: Clone ID: 700899387_FLI
      US-10-425-114-10213

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Query Match	78.4%;	Score 40;	DB 12;	Length 642;
Best Local Similarity	89.6%;	pred. No. 0.012;		
Matches	43;	Conservative	0.012;	

[illegible]

RESULT 14
 US-10-161-927-01
 / Sequence 81 Application US/10161927-01
 / Publication No. US2003023582A1
 GENERAL INFORMATION:
 / APPLICANT:
 / APPLICANT: Zehnsuen, Bryan D.
 / APPLICANT: Kerkuda, Ramesh
 / APPLICANT: Sphyek, Kimberly A.
 / APPLICANT: Shenoy, Suresh G.
 / APPLICANT: Miller, Charles E.
 / APPLICANT: Hjalte, Torb
 / APPLICANT: Gerlach, Valerie L.
 / APPLICANT: Baumgartner, Jason C.
 / APPLICANT: Guo, Xiaojia
 / APPLICANT: Gannoli, Epha A.
 / APPLICANT: Verner, Corine
 / APPLICANT: Padiguru, Muraidhara
 / APPLICANT: Li, Li
 / APPLICANT: Pena, Carol E.A.
 / APPLICANT: Gorman, Linda
 / APPLICANT: Anderson, David W.
 / APPLICANT: Edinger, Shlomit R.

NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 47
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1089
US-09-533-029-47

Query Match 78.4%; Score 40; DB 10; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 21
US-09-934-455-177

Sequence 177, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:

APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Patentin version 3.1
SEQ ID NO 177
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(2427)
OTHER INFORMATION: G1089
US-09-934-455-177

Query Match 78.4%; Score 40; DB 10; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 22
US-10-225-068-65

Sequence 65, Application US/10225068
Publication No. US20030217383A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.

APPLICANT: Reuber, T. Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E.
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Adam, Luc J.
APPLICANT: Dubell, Arnold T.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
APPLICANT: Brown, Pierre E.
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
FILE REFERENCE: 514442002040
CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(2427)
US-10-225-068-65

Query Match 78.4%; Score 40; DB 15; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 23
US-10-302-267-45

Sequence 45, Application US/10302267
Publication No. US20030229915A1
GENERAL INFORMATION:

APPLICANT: Keddie, James
APPLICANT: Fromm, Michael
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc
APPLICANT: Brown, Pierre
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Samaha, Raymond
APPLICANT: Pilgrim, Marsha
APPLICANT: Creelman, Robert
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REFERENCE: MBI-0007
CURRENT APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/120,880
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: 60/124,278

RESULT 374 US-10-374-780A-229
 Sequence 229, Application US/10374780A
 Publication No. US20040019927A1
 GENERAL INFORMATION:
 APPLICANT: Sherman, Bradley K
 APPLICANT: Riechmann, Jose Luis
 APPLICANT: Jiang, Cai Zhong
 APPLICANT: Heard, Jacqueline E
 APPLICANT: Haake, Volker
 APPLICANT: Creelman, Robert A
 APPLICANT: Ratcliffe, Oliver
 APPLICANT: Adam, Luc J
 APPLICANT: Reuber, T. Lynne
 APPLICANT: Keddie, James
 APPLICANT: Brown, Pierre E
 APPLICANT: Pilgrim, Marsha L
 APPLICANT: Dubell III, Arnold T
 APPLICANT: Pineda, Omaira
 APPLICANT: Yu, Guo-Liang
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
 FILE REFERENCE: MBL-0047 CIP
 CURRENT APPLICATION NUMBER: US/10/374,780A
 CURRENT FILING DATE: 2003-02-25
 PRIOR APPLICATION NUMBER: 09/837,944
 PRIOR FILING DATE: 2001-04-18
 PRIOR APPLICATION NUMBER: 60/310,847
 PRIOR FILING DATE: 2001-08-09
 PRIOR APPLICATION NUMBER: 09/934,455
 PRIOR FILING DATE: 2001-08-22
 PRIOR APPLICATION NUMBER: 60/336,049
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/338,692
 PRIOR FILING DATE: 2001-12-11
 PRIOR APPLICATION NUMBER: 10/171,468
 PRIOR FILING DATE: 2002-06-14
 PRIOR APPLICATION NUMBER: 10/225,066
 PRIOR FILING DATE: 2002-08-09
 PRIOR APPLICATION NUMBER: 10/225,067
 PRIOR FILING DATE: 2002-08-09
 PRIOR APPLICATION NUMBER: 10/225,068

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Query Match      78.4%; Score 40; DB 15; Length 2663;  
Best Local Similarity 89.6%; Pident. No. 0.012;  
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
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Db       865  GATACCAAGATTAGAGAGAGAGAGAGAGAGAGAAAGC 912
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Query Match      78.4% Score 40; DB 14; Length 4236;
Best Local Similarity 89.6%; Pred. No. 0.01;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY          1 GAGGATGAACCTGAAGAAGAGAAAGAGAGAGAGAGAGAGAGAGAG
Db          3299 GAGGAGGAAAGAAAGAGAGAGAGAAAGAAAGAGAGAGAGAG
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US-10-128-714-5204
Sequence 5204, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Weng
APPLICANT: Tiebkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Ertosmkln, Alexey M

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C 135	35.4	69.4	124310	4	BX324144	
C 136	35.4	69.4	124310	4	BX324144	
C 137	35.4	69.4	124310	4	BX324144	
C 138	35.4	69.4	124310	4	BX324144	

ORGANISM

Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCES

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 22842)
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)

REFERENCES

2 (bases 1 to 22842)
Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doeber,A.

JOURNAL

The sequence of Homo sapiens BAC clone RP11-139J6
Unpublished (2001)

AUTHORS

3 (bases 1 to 22842)
Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doeber,A.

JOURNAL

4 (bases 1 to 22842)
Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doeber,A.

REFERENCES

Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

AUTHORS

5 (bases 1 to 22842)
Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doeber,A.

JOURNAL

Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCES

6 (bases 1 to 22842)
Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doeber,A.

AUTHORS

Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916188.

JOURNAL

Genome Center
Center: Washington University Genome Sequencing Center
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
Center project name: H_NH0139J06
Drafting Center: WIBR

COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Moon,P.Y., Zhao,B., Fritgen,E., Tareno,M., Cataneese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong

and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574017, 2000 bp overlap.
Actual end of this clone is at base position 4899 of RP11-574017.

Polymorphisms have been identified between AC013272 and AC092603.

FEATURES

The sequence of AC073396 has been incorporated into AC092603.

Source

Location/Qualifiers

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="2"

/map="2"

/clone="RP11-139J6"

/clone_id="RP11-139J6"

352..465

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1377..1424

/rpt_family="(TG)n"

1424..1449

/rpt_family="(GA)n"

1485..1665

/rpt_family="Alu"

1669..1966

/rpt_family="Alu"

2812..2918

/rpt_family="MIR"

3183..3448

/rpt_family="CT-rich"

5541..5566

/rpt_family="AT-rich"

5576..5870

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5873..6183

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6195..6301

/rpt_family="MIR"

6627..6733

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7278..7415

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7638..7723

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8140..8218

/rpt_family="G-rich"

8663..8922

/rpt_family="MIR"

9191..9346

/rpt_family="MIR"

10172..10296

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10436..10550

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11016..11169

/rpt_family="MIR"

11617..11882

/rpt_family="L2"

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/note="match to EST AA887330 (NID:93002438) of 40h05.b1"

12378..12902

/note="match to EST A1791589 (NID:95339305) of 40h05.y5"

13059

/note="match to EST BF475329 (NID:911546156)"

13072..13459

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14030..14244

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(NID:G12886265)"
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(NID:G12933576)"
repeat_region
14413..14439
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14762..14822
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(NID:G12877089)"
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/note="similar to Homo sapiens EST AL544609
(NID:G12877089)"
misc_feature
15084..15487
/note="similar to Sus scrofa EST AW785035 (NID:g7841811)"
misc_feature
15110..15648
/note="similar to Rattus norvegicus EST AW916723
(NID:G8082456)"
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15747..15832
/rpc_family="G-rich"
repeat_region
18481..18596
/rpc_family="L2"
repeat_region
19266..19675
/rpc_family="L2"
repeat_region
20027..20223
/rpc_family="MER1_type"
repeat_region
20315..20416
/rpc_family="L2"
repeat_region
20537..20973
/rpc_family="L2"
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22057..22471
/note="match to EST AA830781 (NID:g2903880) cc56p01.g1"
misc_feature
22057..22208
/note="match to EST AA836522 (NID:g2910841) cd22a08.g1"
ORIGIN
Query Match 100.0%; Score 51; DB 9; Length 22842;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCAG 51
Db 14451 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCAG 14401
RESULT 6
PVI251176 1168 bp DNA linear MAM 01-JUN-2001
LOCUS Phoca vitulina partial aar2b gene for alpha adrenergic receptor 2B.
DEFINITION AJ251176
VERSION AJ251176.1 GI:11322419
KEYWORDS aar2b gene; alpha adrenergic receptor 2B.
SOURCE Phoca vitulina (harbor seal)
ORGANISM Phoca vitulina
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Carnivora; Pinnipedia; Phocidae; Phoca.
Madsen, O., Scally, M., Douady, C. J., Kao, D. J., Debry, R. W., Adkins, R.,
Amarine, H. M., Stanhope, M. J., de Jong, W. W. and Springer, M. S.
Parallel adaptive radiations in two major clades of placental
mammals
JOURNAL Nature 409 (6820), 610-614 (2001)
MEDLINE 21082081
PUBMED 11214318
REFERENCE 2 (bases 1 to 1168)
AUTHORS Madsen, O.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-1999) Madsen O., Department of Biochemistry,
```

```
University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
NETHERLANDS
FEATURES
source
Location/Qualifiers
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/organism="Phoca vitulina"
/mol_type="genomic DNA"
/db_xref="taxon:9720"
1..1168
/gene="aar2b"
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/codon_start=2
/product="alpha adrenergic receptor 2B"
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/db_xref="GI:11322420"
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/db_xref="SPTREMBL:O9GL07"
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DIVATLILPFLANBLGWYFRRTWCVYALDVLFTSSIVHLCAISLDRYMAYV
PALEVNSKRTPRKICITLITWLIAAVLSPLIKYKGGQPGAPAGPOCKNOEMAYI
LASISGFPAPCLIMILYLRITYLAKSHRRGPRKAGPGSGESKPSVPTGSTK
LPTLASLASEBANGHSKPTGKEGDTPEPDPALPWSALPSSGOSQKXGVCAS
PEEABEEBEEBEEBCEPQALPSPASACSPPLPQPGSVLVLATLKGVLGAGVGTAS
GQWRRRRRLQTLREKRFTEVLAVIVGVLCMPFFFSYSIGAIQPHCKVPHGLF"
ORIGIN
Query Match 90.6%; Score 46.2; DB 4; Length 1168;
Best Local Similarity 94.1%; Pred. No. 0.0017;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCAG 51
Db 833 GAGGAGGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCTCAG 883
RESULT 7
LPA505821 1180 bp DNA linear MAM 12-DEC-2002
LOCUS Lama pacos partial adra2b gene for alpha 2B adrenergic receptor,
dra2b-2 allele.
ACCESSION AJ505821
VERSION AJ505821.1 GI:22324219
KEYWORDS adra2b gene; alpha 2B adrenergic receptor.
SOURCE Lama pacos (alpaca)
ORGANISM Lama pacos
Eukaryota; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
Madsen, O., Willemssen, D., Ursing, B. M., Arnason, U. and de Jong, W. W.
Molecular evolution of the mammalian alpha 2B adrenergic receptor
Mol. Biol. Evol. 19 (12), 2150-2160 (2002)
MEDLINE 22337198
PUBMED 12446807
REFERENCE 2
Madsen, O., Willemssen, D., Ursing, B. M., Arnason, U. and de Jong, W. W.
Molecular evolution of the alpha 2B adrenergic receptor
JOURNAL Unpublished
AUTHORS Madsen, O.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2002) Madsen O., 161 Biochemistry NMI, University
of Nijmegen, PO.BOX 9101, 6500HB Nijmegen, NETHERLANDS
FEATURES
source
Location/Qualifiers
1..1180
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/db_xref="taxon:30538"
2..1180
/gene="adra2b"
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/gene="adra2b"
/codon_start=1
/allele="adra2b-2"
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Query Match	76.1%	Score 38.8	DB 10	Length 1347
Best Local Similarity	86.0%	Pred. No. 0.23		
Matches 43	Conservative 0	Mismatches 7	Indels 0	Gaps 0

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM
AF332050	Mus musculus strain ILS adrenergic receptor alpha 2B (Adra2b) mRNA, complete cds.	AF332050	GI:14193667	Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1347)	Erhinger, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Camniff, J., Beeson, M., Gordon, L., Bennett, B., Johnson, T.E. and Skela, J.M.	High-throughput sequence identification of gene coding variants within alcohol-related QTLs

JOURNAL	MEDLINE	PUBMED
2 (bases 1 to 1347)	Erhinger, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Camniff, J., Beeson, M., Gordon, L., Bennett, B., Johnson, T.E. and Skela, J.M.	Submitted (26-DEC-2000)

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1..1347	/gene="Adra2b"
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/product="adrenergic receptor alpha 2B"	
/protein_id="AAK56079.1"	
/db_xref="GI:14193668"	
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LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM
AF332050	Mus musculus strain ILS adrenergic receptor alpha 2B (Adra2b) mRNA, complete cds.	AF332050	GI:14193667	Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1347)	Erhinger, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Camniff, J., Beeson, M., Gordon, L., Bennett, B., Johnson, T.E. and Skela, J.M.	Submitted (26-DEC-2000)

JOURNAL	MEDLINE	PUBMED
2 (bases 1 to 1347)	Erhinger, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Camniff, J., Beeson, M., Gordon, L., Bennett, B., Johnson, T.E. and Skela, J.M.	Submitted (26-DEC-2000)

FEATURES	source
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	/strain="ILS"
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/protein_id="AAK56079.1"	
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/translation="MVHDEPYSVQATAIAISATIFLLIFTEIGNALVILAVTSRSLR APQALFLVLSAADILVATLIIPELSNELGIVYFPRMCEVIALADVCTSSIVH LCAISLDPRVMSADILEVNSKRTPRRIICILITWLLAAVSLPPLIYKGPQREPHGS LPQELNDEAVYIIAASISGFPAFLIMILVLLIYIAKRSKRGAKRGSGEGSS KKPRHAGNEVPAASAKVPTIVSPILSVGANHPKPREKGGTPEDEARALPNNHS ALPSPVODKKGTGATAEKAEDEEVECEPQILPASPASVFNPLQDQTSRVLV ATLGGQVLLSKNVGASGQWRRRTQLSRERFLVLAIVGIVVCMPEPFPSYSGG AICPHCKVPHGLFQFPFMWIGYCNSSINPIYITIFNDFRRAFRRIICROWTQGW"	

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KEYWORDS      L00979.1 GI:191547
VERSION       alpha-2 adrenergic receptor.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     Chrusciński, A.U., Link, R.E., Daunt, D.A., Barsh, G.S. and
AUTHORS       Kodilla, B.K.
TITLE         Cloning and expression of the mouse homolog of the human alpha 2-C2
JOURNAL       Biochem. Biophys. Res. Commun. 186 (3), 1280-1287 (1992)
MEDLINE       92378586
PUBMED        1354956
COMMENT       source text: Mus musculus (strain 129/Sv) DNA.
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LCASIDRVAWSRALEYNRSKRTPRIKCIILTWMLAAVISLPLLKYKDORPEHG
LPQOENLOEAMVLIASISGSPAPCLIMLVIRIYIARSHRGAGARGSGEGSS
KKPRRAGCYPAPKAAPTIVSYPLSSVGEAAGHVPPREKEGETPEPARALPPNS
KLPPSVDDKKGTSGATAEKGAEEDEVEECEDQTLPASPASTVFNPLODQRSTVL
ATIRGVLTLSKNVGASGWMMRRQTQSREKRTFLVAVIIGFVVCWFPPFSYSLG
AICPHCKVPHGLGFQFFFWIGYCNSINPIYITIFNDFRFAFRRLICROMTQGM"

ORIGIN
Query Match          76.1%; Score 38.8; DB 10; Length 1650;
Best Local Similarity 86.0%; Pred. No. 0.23;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy      1 GAGCATGAGCTGAAGAAGAGAGAGAGAGAGAGAGAGGTGAACCCCA 50
        |||
Db      1109 GAGAAAGGAGCTGAAGAGATGAAGAGAGAGAGGTGAAGATTGACCACA 1158

RESULT 24
BATA2BR    BATA2BR           2319 bp      mRNA      linear      ROD 27-APR-1993
LOCUS      Rat alpha-2B-adrenergic receptor (RNG-alpha-2) mRNA, complete cds.
DEFINITION
ACCESSION   M32061
VERSION     M32061.1 GI:202589
KEYWORDS    adrenergic receptor.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 2319)
Zeng,D.W., Harrison,J.K., D'Angelo,D.D., Barber,C.M., Tucker,A.L.,
Lu,Z.H. and Lynch,K.R.
Molecular characterization of a rat alpha 2B-adrenergic receptor
Proc. Natl. Acad. Sci. U.S.A. 87 (8), 3102-3106 (1990)
90222177
2158103
Original source text: Rat (strain Sprague Dawley) adult kidney,
cDNA to mRNA, clones dz-(3,5,6).
Direct entry and computer-readable sequence [1] kindly submitted by
K.R. Lynch, 12-FEB-1990.
location/Qualifiers
1..2319
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 /mol_type="mRNA"
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Massey, E., Mawhney, E., McLeod, M. P., Meador, M., Mei, G., Meeker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nookankoo, S., Ogun, M., Okunodu, G., Oksanen, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peeters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rivers, A., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostrati, N., Sibson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabot, P., Tamerisa, A., Tamerisa, K., Tang, H., Tamsai, J., Taylor, C., Taylor, T., Teifrod, B., Thomas, N., Thomas, S., Umanai, K., Vazquez, L., Ver, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

2 (bases 1 to 261258)
 Direct Submission
 Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 261258)
 Worley, K.C.
 Direct Submission
 Submitted (10-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Oct 10, 2002 this sequence version replaced gi:21953942. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/atl/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: TUEV
 Center clone name: CH230-1A10
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 190889 bases at least Q40
 Consensus quality: 198612 bases at least Q20
 Consensus quality: 203158 bases at least Q20
 Estimated insert size: 183632; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_dirft_data.html)
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 4484: contig of 4484 bp in length
 * 4485 4484: gap of unknown length
 * 4585 15356: contig of 10772 bp in length
 * 15357 15456: gap of unknown length

FEATURES	source
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*	/organism="Rattus norvegicus"
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*	/db_xref="taxon:10116"
*	/clone="CH230-1A10"
*	1. .1039
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misc_feature	4585. .5659
misc_feature	/note="wgs end_extension clone_end:Sp6"
misc_feature	15457. .16493
misc_feature	/note="wgs end_extension clone_end:Sp6"
misc_feature	47075. .48409
misc_feature	/note="wgs end_extension clone_end:Sp6"
misc_feature	95699. .95814
misc_feature	/note="clone_boundary clone_end:Sp6"
misc_feature	site:EcORI
misc_feature	end_sequence:BH273949"
misc_feature	complement(98888..99662)
misc_feature	/note="clone_boundary clone_end:T7"
misc_feature	site:EcORI
misc_feature	end_sequence:BH273948"
misc_feature	complement(99327..99667)
misc_feature	/note="clone_boundary clone_end:T7"
misc_feature	site:EcORI
misc_feature	end_sequence:BH273948"
misc_feature	119027. .120093
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misc_feature	145590. .147159
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misc_feature	150738. .152121
misc_feature	/note="wgs end_extension clone_end:T7"

RESULT 30
AC112830

DEFINITION	Rattus norvegicus clone CH230-46115, ***	2/8543 DP	DNA	linear	HTG 21-SEP-2002
ACCESSION	AC112830	***	2 unordered pieces.	SEQUENCING IN PROGRESS	

ACCESSION	AC112830
VERSION	AC112830.3
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus

REFERENCES
AUTHORS

REFERENCE

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

AUTHORS

1 (bases 1 to 276543)

Murphy, D. W.

TITLE
JOURNAL

REFERENCE 2 (bases 1 to 276543)
AUTHORS Morley, K.C.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2002) Human Genome Sequencing Center

REFERENCE
AUTHORS
TITLE
JOURNAL

3 (baees 1 to 276543)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (21-SEP-2002) Human Genome Sequencing Consortium

COMMENT

of Molecular and Human Genetic Genome Sequencing Center, Department Baylor Plaza, Houston, TX 77030, USA

On Sep 21, 2002 this sequence version replaced gi:21743229.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Arlas (<http://www.hgisec.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hpsc.bcm.tmc.edu/>
Contact: hpsc-help@bcm.tmc.edu
Project Information
Center project name: GRPQ
Center clone name: CH20-46115

assembly program: Phrap; version 0.990329
 Consensus quality: 237012 bases at least Q40
 Consensus quality: 233346 bases at least Q30
 Consensus quality: 240985 bases at least Q20
 Estimated insert size: 252028; sum-of-contigs
 Quality coverage: 5x in Q20 bases; sum-of-

NOTE: Estimated insert size may differ from sequence length (see http://www.hpsc.bcm.tmc.edu/docs/Genbank_draft_date.html). NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES

Source

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misc_feature

misc_feature

misc_feature

misc_feature

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270664. .272163
/note="wgs_end_extension
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Page 17

Page 17

Page 17

Page 17

Page 17

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FT FT /*tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence is deleted for a 9 nucleotide
FT polymorphic site found at nucleotides 901-909 of the
FT wildtype alpha-2BAR protein (AA199905)"
XX XX
XX WO200179561-A2.
XX PD 25-OCT-2001.
XX PF 17-APR-2001; 2001WO-US012575.
XX PR 17-APR-2000; 2000US-00551744.
XX PR 10-AUG-2000; 2000US-00636259.
XX PR 19-OCT-2000; 2000US-00692077.
XX PA (LIGC/) LIGGETT S B.
XX PA (SMAL/) SMAL K M.
XX PI Liggett SB, Small KM;
XX DR WPI: 2001-611728/70.
XX DR P-PSDB; AAMS2118.
XX PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX PT determining whether an individual is at increased risk of developing a
XX PT disease associated with the corresponding receptor comprises detecting a
XX PT polymorphic site.
XX PS Claim 5; Page 144-145; 163pp; English.
XX XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX CC receptor gene (I)-(III) by detecting a polymorphic site, comprising: (a)
XX CC obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A
XX CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic
XX CC site comprising nucleotide positions 901-909 of (I), a site comprising
XX CC cytosine or guanine at position 753 of (II) or a site comprising (A)
XX CC (GGGGCGGGGCG) or (B) (GGGGGGGCGG) at positions 961-972 of (III). The
XX CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor
XX CC gene and further used to determine whether an individual is at increased
XX CC risk of developing a disease associated with alpha2B, alpha2A or alpha2,
XX CC comprising detecting a polymorphic site which correlate to disease
XX CC selected from cardiovascular disease, central nervous system disease and
XX CC combinations of these. In addition, the technique may be used to predict
XX CC an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g.
XX CC epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
XX CC UK1304, BHT933 and combinations of these) or antagonist (e.g. yohimbine,
XX CC prazosin, ARC 239, rauvolfine, idazoxan, tolazoline, phenclamine and
XX CC combinations of these) by detecting the polymorphic site and correlating
XX CC the site to a predetermined response (where the response is correlated to
XX CC adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
XX CC phosphatase levels). The present sequence is that of the third
XX CC intracellular loop of the human alpha-2BAR variant, the sequence is
XX CC deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909
XX CC of the wildtype gene (AA199905)
XX SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 U; 0 Other;
XX XX
XX Query Match 100.0%; Score 51; DB 4; Length 1344;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-05;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 04-JUL-2001 (first entry)
XX XX
XX Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
XX DE Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
XX KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX KW acute myocardial infarction; AMI; Prinzmetal's variant; de.
XX XX
XX Homo sapiens.
XX OS
XX XX
XX Key Location/Qualifiers
XX FT 1. 1344
XX FT CDS
XX FT /*tag= a
XX FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
XX FT variant protein"
XX XX
XX WO200129082-A1.
XX XX
XX PD 26-APR-2001.
XX PF 20-OCT-2000; 2000WO-FI000913.
XX PF 22-OCT-1999; 99US-00422985.
XX PR (JUVNA-) JUVANTIA PHARMA LTD OY.
XX PA Snapiir A, Heinonen P, Alhopuro P, Karyonen M, Koulu M, Pesonen U;
XX PI Scheinin M, Salonen JT, Tuominen T, Lakka TA, Nyysönen K;
XX PI Salonen R, Kauphanen J, Valkonen V;
XX DR WPI: 2001-300318/31.
XX DR P-PSDB; AAE00989.
XX XX
XX New DNA molecule encoding variant specific adrenoceptor protein with
XX PT deletion of specific amino acids located in the third intracellular loop
XX PT of the polypeptide, for treating vascular contraction of coronary
XX PT arteries.
XX XX
XX Claim 3; Page 24-26; 37pp; English.
XX PS The present sequence is a gene encoding human alpha2B-adrenoceptor
XX CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
XX CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
XX CC 18 amino acids (amino acids 294-311), located in the third intracellular
XX CC loop of the receptor polypeptide. The variant is obtained by deletion of
XX CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
XX CC gene is located on chromosome 2. Alpha2-AR mediate many of the
XX CC physiological effects of the catecholamines, norepinephrine and
XX CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
XX CC a mammal suffering from vascular contraction of coronary arteries and a
XX CC disease involving vascular contraction of coronary arteries which is
XX CC clinically expressed as coronary heart disease (CHD), unstable chronic
XX CC angina pectoris which is clinically expressed as Prinzmetal's variant
XX CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
XX CC gene therapy
XX XX
XX SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 U; 0 Other;
XX XX
XX Query Match 93.7%; Score 47.8; DB 5; Length 1344;
XX Best Local Similarity 96.1%; Pred. No. 0.00057;
XX Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
AAD04761
ID AAD04761 standard; DNA; 1344 BP.
XX AC AAD04761;
XX XX

RESULT 4
AAD4388
ID AAD4388 standard; DNA; 1344 BP.
XX XX

PA (EPIC-) EPIDEMIOLOGY AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene.
XX
PS Claim 1; Page 40-44; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviours in schizophrenia
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA
XX
SQ Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 0 U; 1 Other;
XX
Query Match 82.0%; Score 41.8; DB 6; Length 6904;
Best Local Similarity 95.6%; Pred. No. 0.025;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTAA 45
|||||
DB 5880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTAA 5924
|||||
RESULT 7
AA199905
ID AA199905 standard; DNA; 1353 BP.
XX
AC AA199905;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR;
KW GenBank Accession AF009500; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence includes a 9 nucleotide polymorphic site
FT at nucleotides 901-909 absent in the alpha-2BAR variant
FT (AA199906)"
XX
XX WO200179561-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 17-APR-2001; 2001WO-US012575.
XX
XX PR 17-APR-2000; 2000US-00551744.
XX PR 10-AUG-2000; 2000US-00636259.
XX PR 19-OCT-2000; 2000US-00692077.

XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
XX
DR P-PSDB; AAM52117.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting a
PT polymorphic site.
XX
PS Claim 4; Page 144; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising: (a)
CC obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A
CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic
CC site comprising nucleotide positions 901-909 of (I), a site comprising
CC cytosine or guanine at position 753 of (II) or a site comprising (A)
CC (9999CG9999CG) or (B) (9999CG9999CG) at positions 961-972 of (III). The
CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor
CC gene and further used to determine whether an individual is at increased
CC risk of developing a disease associated with alpha2B, alpha2A or alpha2,
CC comprising detecting a polymorphic site which correlate to disease
CC selected from cardiovascular disease, central nervous system disease and
CC combinations of these. In addition, the technique may be used to predict
CC an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g.
CC epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
CC UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine,
CC prazosin, ARC 239, rauwolfine, idazoxan, tolazoline, phentolamine and
CC combinations of these) by detecting the polymorphic site and correlating
CC the site to a predetermined response (where the response is correlated to
CC adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
CC phosphate levels). The present sequence is that of the third
CC intracellular loop of the human alpha-2BAR (GenBank Accession AF009500);
CC the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-
CC 909, absent in the alpha-2BAR variant (AA199906)
XX
SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;
XX
Query Match 81.6%; Score 41.6; DB 4; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.026;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTAA 51
|||||
DB 892 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTAA 939
|||||
RESULT 8
AAD04762
ID AAD04762 standard; DNA; 1353 BP.
XX
AC AAD04762;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a

CC antigen to raise anti-DNA antibodies or to elicit another immune
CC response, and for identifying polynucleotides encoding the other protein
CC with which binding occurs or to identify inhibitors of the binding
CC interaction. The polypeptides may be used to raise antibodies or to
CC elicit immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as a marker for
CC host tissues in which pathogenic organisms invade or reside, and to
CC isolate correlative receptors or ligands in the case of virulence
CC factors. This polynucleotide sequence represents one of the essential
CC genes of *Aspergillus fumigatus* of the invention
XX
SQ Sequence 4367 BP; 1103 A; 1135 C; 1218 G; 911 T; 0 U; 0 Other;
Query Match 70.6%; Score 36; DB 7; Length 4367;
Beet Local Similarity 88.6%; Pred. No. 0.9; Mismatches 0; Gaps 0;
Matches 39; Conservative 0; Indels 0; Gaps 0;
Qy 1 GAGGATGAACTGAGAGGAGGAGGAGGAGGAGGAGTGTGA 44
Db 3314 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTTTGA 3357
RESULT 19
AAC54146/C
ID AAC54146 standard; DNA; 1429 BP.
XX
AC AAC54146;
XX
DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 76850.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 76850.
XX
XX Hybridization assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX
XX 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
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PR 08-APR-1999; 99US-0128714P.
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PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 20-JUL-1999; 99US-0144884P.
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PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145513P.
PR 27-JUL-1999; 99US-0145518P.
PR 27-JUL-1999; 99US-0145519P.
PR 28-JUL-1999; 99US-0145591P.

Query Match	68.64;	Score 35;	DB 3;	Length 1429;
Best Local Similarity	88.48;	Pred. NO. 1.6;		
Matches	38;	Conservative	0. Mismatch	

RESULT 20
AAQ88817
ID AAQ88817 standard; cDNA; 1820 BP
XX

AAQ88817;

25-MAR-2003 (revised)
09-OCT-1995 (first entry)
XX

Human surfactant protein A receptor (hSPAR) cDNA

Homo sapiens.

WO9506665-A1.

30-AUG-1994; 94WO-US009752.

30-DEC-1993; 93US-00114951.
93US-00176218.

(VOICE) UNIV JEFFERSON THOMAS.

scrayer DS, Chander A;

P-PSDB; AAR71460

Compsn. capable of binding to surfactant protein-A receptor - which modulates secretion of alveolar surfactant, e.g. to treat respiratory distress syndrome.

-----; page 35-36; 53pp; English

but principally in their α -spiral CUNs were compared. They are highly homologous, divergent. The 32.3 kDa human and 32.8 kDa porcine ORFs are similar. Both show structural features consistent with cell membrane bound receptors. The projected secondary structure of hSPAR ORF is similar to that of its porcine counterpart. The SPAR protein is predicted to have a hydrophobic α -helix of 28 residues beginning at AA 48. It is followed by a second α helix of 24 residues beginning at AA 48. It is followed by a third α helix of 24 residues beginning at AA 100. It is followed by a fourth α helix of 24 residues beginning at AA 128. It is followed by a fifth α helix of 24 residues beginning at AA 156. It is followed by a sixth α helix of 24 residues beginning at AA 184. It is followed by a seventh α helix of 24 residues beginning at AA 212. It is followed by an eighth α helix of 24 residues beginning at AA 240. It is followed by a ninth α helix of 24 residues beginning at AA 268. It is followed by a tenth α helix of 24 residues beginning at AA 296. It is followed by an eleventh α helix of 24 residues beginning at AA 324. It is followed by a twelfth α helix of 24 residues beginning at AA 352. It is followed by a thirteenth α helix of 24 residues beginning at AA 380. It is followed by a fourteenth α helix of 24 residues beginning at AA 408. It is followed by a fifteenth α helix of 24 residues beginning at AA 436. It is followed by a sixteenth α helix of 24 residues beginning at AA 464. It is followed by a seventeenth α helix of 24 residues beginning at AA 492. It is followed by an eighteenth α helix of 24 residues beginning at AA 520. It is followed by a nineteenth α helix of 24 residues beginning at AA 548. It is followed by a twentieth α helix of 24 residues beginning at AA 576. It is followed by a twenty-first α helix of 24 residues beginning at AA 604. It is followed by a twenty-second α helix of 24 residues beginning at AA 632. It is followed by a twenty-third α helix of 24 residues beginning at AA 660. It is followed by a twenty-fourth α helix of 24 residues beginning at AA 688. It is followed by a twenty-fifth α helix of 24 residues beginning at AA 716. It is followed by a twenty-sixth α helix of 24 residues beginning at AA 744. It is followed by a twenty-seventh α helix of 24 residues beginning at AA 772. It is followed by a twenty-eighth α helix of 24 residues beginning at AA 800. It is followed by a twenty-ninth α helix of 24 residues beginning at AA 828. It is followed by a thirtieth α helix of 24 residues beginning at AA 856. It is followed by a thirty-first α helix of 24 residues beginning at AA 884. It is followed by a thirty-second α helix of 24 residues beginning at AA 912. It is followed by a thirty-third α helix of 24 residues beginning at AA 940. It is followed by a thirty-fourth α helix of 24 residues beginning at AA 968. It is followed by a thirty-fifth α helix of 24 residues beginning at AA 996. It is followed by a thirty-sixth α helix of 24 residues beginning at AA 1024. It is followed by a thirty-seventh α helix of 24 residues beginning at AA 1052. It is followed by a thirty-eighth α helix of 24 residues beginning at AA 1080. It is followed by a thirty-ninth α helix of 24 residues beginning at AA 1108. It is followed by a fortieth α helix of 24 residues beginning at AA 1136. It is followed by a forty-first α helix of 24 residues beginning at AA 1164. It is followed by a forty-second α helix of 24 residues beginning at AA 1192. It is followed by a forty-third α helix of 24 residues beginning at AA 1220. It is followed by a forty-fourth α helix of 24 residues beginning at AA 1248. It is followed by a forty-fifth α helix of 24 residues beginning at AA 1276. It is followed by a forty-sixth α helix of 24 residues beginning at AA 1304. It is followed by a forty-seventh α helix of 24 residues beginning at AA 1332. It is followed by a forty-eighth α helix of 24 residues beginning at AA 1360. It is followed by a forty-ninth α helix of 24 residues beginning at AA 1388. It is followed by a fiftieth α helix of 24 residues beginning at AA 1416. It is followed by a fifty-first α helix of 24 residues beginning at AA 1444. It is followed by a fifty-second α helix of 24 residues beginning at AA 1472. It is followed by a fifty-third α helix of 24 residues beginning at AA 1500. It is followed by a fifty-fourth α helix of 24 residues beginning at AA 1528. It is followed by a fifty-fifth α helix of 24 residues beginning at AA 1556. It is followed by a fifty-sixth α helix of 24 residues beginning at AA 1584. It is followed by a fifty-seventh α helix of 24 residues beginning at AA 1612. It is followed by a fifty-eighth α helix of 24 residues beginning at AA 1640. It is followed by a fifty-ninth α helix of 24 residues beginning at AA 1668. It is followed by a sixtieth α helix of 24 residues beginning at AA 1696. It is followed by a sixty-first α helix of 24 residues beginning at AA 1724. It is followed by a sixty-second α helix of 24 residues beginning at AA 1752. It is followed by a sixty-third α helix of 24 residues beginning at AA 1780. It is followed by a sixty-fourth α helix of 24 residues beginning at AA 1808. It is followed by a sixty-fifth α helix of 24 residues beginning at AA 1836. It is followed by a sixty-sixth α helix of 24 residues beginning at AA 1864. It is followed by a sixty-seventh α helix of 24 residues beginning at AA 1892. It is followed by a sixty-eighth α helix of 24 residues beginning at AA 1920. It is followed by a sixty-ninth α helix of 24 residues beginning at AA 1948. It is followed by a seventieth α helix of 24 residues beginning at AA 1976. It is followed by a seventy-first α helix of 24 residues beginning at AA 2004. It is followed by a seventy-second α helix of 24 residues beginning at AA 2032. It is followed by a seventy-third α helix of 24 residues beginning at AA 2060. It is followed by a seventy-fourth α helix of 24 residues beginning at AA 2088. It is followed by a seventy-fifth α helix of 24 residues beginning at AA 2116. It is followed by a seventy-sixth α helix of 24 residues beginning at AA 2144. It is followed by a seventy-seventh α helix of 24 residues beginning at AA 2172. It is followed by a seventy-eighth α helix of 24 residues beginning at AA 2200. It is followed by a seventy-ninth α helix of 24 residues beginning at AA 2228. It is followed by an eightieth α helix of 24 residues beginning at AA 2256. It is followed by an eighty-first α helix of 24 residues beginning at AA 2284. It is followed by an eighty-second α helix of 24 residues beginning at AA 2312. It is followed by an eighty-third α helix of 24 residues beginning at AA 2340. It is followed by an eighty-fourth α helix of 24 residues beginning at AA 2368. It is followed by an eighty-fifth α helix of 24 residues beginning at AA 2396. It is followed by an eighty-sixth α helix of 24 residues beginning at AA 2424. It is followed by an eighty-seventh α helix of 24 residues beginning at AA 2452. It is followed by an eighty-eighth α helix of 24 residues beginning at AA 2480. It is followed by an eighty-ninth α helix of 24 residues beginning at AA 2508. It is followed by a ninetieth α helix of 24 residues beginning at AA 2536. It is followed by a ninety-first α helix of 24 residues beginning at AA 2564. It is followed by a ninety-second α helix of 24 residues beginning at AA 2592. It is followed by a ninety-third α helix of 24 residues beginning at AA 2620. It is followed by a ninety-fourth α helix of 24 residues beginning at AA 2648. It is followed by a ninety-fifth α helix of 24 residues beginning at AA 2676. It is followed by a ninety-sixth α helix of 24 residues beginning at AA 2704. It is followed by a ninety-seventh α helix of 24 residues beginning at AA 2732. It is followed by a ninety-eighth α helix of 24 residues beginning at AA 2760. It is followed by a ninety-ninth α helix of 24 residues beginning at AA 2788. It is followed by a hundredth α helix of 24 residues beginning at AA 2816. It is followed by a hundred-first α helix of 24 residues beginning at AA 2844. It is followed by a hundred-second α helix of 24 residues beginning at AA 2872. It is followed by a hundred-third α helix of 24 residues beginning at AA 2900. It is followed by a hundred-fourth α helix of 24 residues beginning at AA 2928. It is followed by a hundred-fifth α helix of 24 residues beginning at AA 2956. It is followed by a hundred-sixth α helix of 24 residues beginning at AA 2984. It is followed by a hundred-seventh α helix of 24 residues beginning at AA 3012. It is followed by a hundred-eighth α helix of 24 residues beginning at AA 3040. It is followed by a hundred-ninth α helix of 24 residues beginning at AA 3068. It is followed by a hundred-tenth α helix of 24 residues beginning at AA 3096. It is followed by a hundred-eleventh α helix of 24 residues beginning at AA 3124. It is followed by a hundred-twelfth α helix of 24 residues beginning at AA 3152. It is followed by a hundred-thirteenth α helix of 24 residues beginning at AA 3180. It is followed by a hundred-fourteenth α helix of 24 residues beginning at AA 3208. It is followed by a hundred-fifteenth α helix of 24 residues beginning at AA 3236. It is followed by a hundred-sixteenth α helix of 24 residues beginning at AA 3264. It is followed by a hundred-seventeenth α helix of 24 residues beginning at AA 3292. It is followed by a hundred-eighteenth α helix of 24 residues beginning at AA 3320. It is followed by a hundred-nineteenth α helix of 24 residues beginning at AA 3348. It is followed by a hundred-twentieth α helix of 24 residues beginning at AA 3376. It is followed by a hundred-twenty-first α helix of 24 residues beginning at AA 3404. It is followed by a hundred-twenty-second α helix of 24 residues beginning at AA 3432. It is followed by a hundred-twenty-third α helix of 24 residues beginning at AA 3460. It is followed by a hundred-twenty-fourth α helix of 24 residues beginning at AA 3488. It is followed by a hundred-twenty-fifth α helix of 24 residues beginning at AA 3516. It is followed by a hundred-twenty-sixth α helix of 24 residues beginning at AA 3544. It is followed by a hundred-twenty-seventh α helix of 24 residues beginning at AA 3572. It is followed by a hundred-twenty-eighth α helix of 24 residues beginning at AA 3600. It is followed by a hundred-twenty-ninth α helix of 24 residues beginning at AA 3628. It is followed by a hundred-thirtieth α helix of 24 residues beginning at AA 3656. It is followed by a hundred-thirty-first α helix of 24 residues beginning at AA 3684. It is followed by a hundred-thirty-second α helix

Sequence 1820 BP: 501 A: 303 C 473 T

68 68: 688 32

Species	Conservative	Misclassified	Pred. No. 1.6
38; Conservative	88.4%	0%	

[illegible][illegible]

DB 572 GAAGATGATGATGAAGACGAGAGCAAGAAGAAATGTG 614

RESULT 21
ID ABN76609
XX ABN76609 standard; cDNA; 392 BP.
XX AC ABN76609;
XX DE 08-JUL-2002 (first entry)
XX Human ORF1556 cDNA, SEQ ID NO:3111.

KM Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KM disease monitoring; cytokine; cell proliferation; cell differentiation;
KM immune modulation; haematopoiesis regulation; tissue growth;
KM angiogenesis; activin; inhibin; chemotactic; chemokineic; haemostatic;
KM thrombolytic; tumour inhibition; bodily characteristics; fertility;
KM behaviour; cancer; proliferative disorder; neurological disorder;
KM cardiovascular disease; immune system disorder; organ transplantation;
KM tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KM hypothyroidism; cholesterol ester storage disease; infection; vulnerability;
KM vasoregulation; antidiabetic; cytosolic; neotropic;
KM neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KM cardiac; hypotensive; antihypoid; antiinflammatory; immunomodulator;
KM dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.

OS Homo sapiens.
XX MO200190366-A2.
XX PD 29-NOV-2001.
XX PF 24-MAY-2001; 2001WO-US017076.
XX PR 24-MAY-2000; 2000US-0206690P.
XX PA (CUPRA-) CUPAGEN CORP.
XX P1 Leach MD, Shinkets RA;
XX DR WPI; 2002-106200/14.
XX DX P-P5DB; ABP32583.

PT Novel human polypeptides and polymucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation.

PS Claim 1; Page 1036; 2508bp; English.
XX Sequences ABP1028-ABP35561 represent 4534 novel human proteins
XX designated ORF (open reading frame) 1-4534, and sequences ABN75054-
XX ABN75857 represent cDNAs encoding them. The invention also encompasses
XX polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
XX referred to as ORFX) proteins, polymucleotides at least 85% identical to
XX the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
XX polymucleotides, the recombinant production of ORFX proteins, antibodies
XX specific for ORFX proteins, methods of detecting ORFX polymucleotides and
XX polypeptides, methods of screening for modulators of ORFX expression or
XX activity, and methods of screening individuals for a predisposition to an
XX ORFX-associated disorder. The ORFX proteins of the invention have a wide
XX range of biological activities, such as cytokine, cell proliferation,
XX cell differentiation, immune modulation, haematopoiesis regulation,
XX tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
XX chemokinetic activity, haemostatic activity, thrombolytic activity,
XX receptor/ligand, antiinflammatory activity, tumour inhibition activity,
XX and antifibrotic activity, and may also be involved in the determination
XX of bodily characteristics, fertility and behaviour. ORFX proteins,
XX nucleic acids and antibodies may be used in the treatment of cancers,
XX other proliferative disorders such as psoriasis and benign tumours,
XX neurological disorders such as epilepsy and Alzheimer's disease,
XX cardiovascular diseases, immune system disorders, disorders related to

CC	organ transplantation, disorders of tissue growth and regeneration, CC
CC	diseases such as diabetes mellitus, hypothyroidism, and cholesterol, CC
CC	storage disease, and infectious diseases caused by viral, bacterial, CC
CC	fungal and other pathogens. ORFX nucleic acids may also be used as a CC
CC	source of primers and probes, in the detection of ORFX genomic sequences CC
CC	or transcripts, in the identification and cloning of homologous CC
CC	sequences, in genetic diagnosis, and in forensic biology. The ORFX CC
CC	nucleic acids may additionally be used to produce transgenic animals CC
CC	which may be useful for studying the function and/or activity of ORFX CC
CC	protein, and in drug screening. The ORFX proteins may also be used as CC
CC	immunogens to generate specific antibodies, which are useful in the CC
CC	diagnosis, treatment and monitoring of ORFX-associated diseases
XX	
SO	Sequence 392 BP; 116 A; 64 C; 112 G; 100 T; 0 U; 0 Other;
Query Match	67.5%; Score 34.4; DB 6; Length 392;
Best Local Similarity	86.4%; Pred. No. 2.1;
Matches	38; Conservative 0; Mismatches 6; Indels 0; Gaps
Oy	1 GAGGATGAACCTGAGAGGAGGAGGAGGAGGAGGAGGAGTGTGCA 44
Db	85 GAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGA 128
RESULT 22	
AAV25477	
ID	AAV25477 standard; cDNA; 5000 BP.
XX	
AC	AAV25477;
XX	
DT	06-AUG-1998 (first entry)
XX	
DE	Rat sulphonylurea receptor SUR2 encoding cDNA.
XX	
KW	Rat: sulphonylurea receptor; SUR2; hypertension; ischaemia;
XX	
KW	potassium channel disease; ss.
XX	
OS	Rattus sp.
XX	
FT	Key Location/Qualifiers
FT	CDS 271..4908
FT	/*tag= a
FT	/product= "SUR2"
FT	/note= "sulphonylurea receptor"
XX	
PN	JPI0052275-A.
XX	
PD	24-FEB-1998.
XX	
PF	09-AUG-1996; 96JP-00227552.
XX	
PR	09-AUG-1996; 96JP-00227552.
XX	
PA	(KIYO/) KIYONO S.
PA	(NICH-) JAPAN CHEM RES CO LTD.
XX	
DR	WPI: 1998-200632/18.
XX	
DR	P-PSDB; AAW53602.
XX	
PT	New sulphonyl-urea receptor protein - useful for, e.g. diagnosis and
XX	treatment of potassium channel diseases such as ischaemia.
XX	
PS	Claim 2; Fig 7-11; 19pp; Japanese.
XX	
CC	The present sequence encodes a new sulphonylurea receptor (SUR2) protein
CC	isolated from a rat brain cDNA library. The sequence can be derived from
CC	animals such as human or rat. Products of SUR2 can be used for diagnosis
CC	and treatment of potassium channel diseases, e.g. hypertension and
CC	ischaemia
XX	
SO	Sequence 5000 BP; 1238 A; 1287 C; 1243 G; 1232 T; 0 U; 0 Other;
Query Match	67.5%; Score 34.4; DB 2; Length 5000;

CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 6628 BP; 1740 A; 1656 C; 1539 G; 1692 T; 0 U; 1 Other;

Query Match 67.5%; Score 34.4; DB 9; Length 6628;
Best Local Similarity 86.4%; Pred. No. 2.5;
Matches 38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGA 44
Db 3109 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 3152

RESULT 25

ADBS2677 standard; DNA; 6628 BP.

ADBS2677;

04-DEC-2003 (first entry)

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3219.

toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
toxicity marker; toxicity progression; drug screening;

primary rat hepatocyte toxicity modelling; gene; ds.

Rattus norvegicus.

WO2003065993-A2.

14-AUG-2003.

04-FEB-2003; 2003WO-US003482.

04-FEB-2003; 2002US-0353171P.

13-MAR-2002; 2002US-0363534P.

08-APR-2002; 2002US-0370248P.

10-APR-2002; 2002US-0371134P.

10-APR-2002; 2002US-0371135P.

11-APR-2002; 2002US-0371413P.

19-APR-2002; 2002US-0373601P.

19-APR-2002; 2002US-0373602P.

22-APR-2002; 2002US-0374139P.

08-MAY-2002; 2002US-0378370P.

09-MAY-2002; 2002US-0378652P.

09-MAY-2002; 2002US-0378653P.

09-MAY-2002; 2002US-0378655P.

09-JUL-2002; 2002US-0394230P.

09-JUL-2002; 2002US-0394233P.

04-SEP-2002; 2002US-0407688P.

28-JAN-2003; 2003US-0442900P.

(GENE-) GENE LOGIC INC.

Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
Elashoff M;
MPI: 2003-731472/69.

Determining if a compound induces a toxic effect on a tissue or cell, for
identifying hepatotoxic compounds, comprises comparing a gene expression
profile of a tissue or cell sample to a database of Tox mean and non-Tox
mean values.

Claim 44; SEQ ID NO 3219; 874pp; English.

The present invention describes a method for determining whether a
compound induces a toxic effect on a tissue or cell. The method comprises
preparing a gene expression profile of a tissue or cell sample exposed to

CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

XX Sequence 6628 BP; 1740 A; 1656 C; 1539 G; 1692 T; 0 U; 1 Other;

Query Match 67.5%; Score 34.4; DB 9; Length 6628;
Best Local Similarity 86.4%; Pred. No. 2.5;
Matches 38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 44
Db 3109 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 3152

RESULT 26

AAQ29703 standard; DNA; 5125 BP.

AAQ29703;

25-MAR-2003 (revised)

17-MAR-1993 (first entry)

IRS-1.

Insulin receptor substrate-1; IRS-1; probe; vector; transform;

IRS-1 metabolism; insulin related disease; ss.

Rattus rattus.

WO9213083-A1.

06-AUG-1992.

17-JAN-1992; 92WO-US000437.

18-JAN-1991; 91US-00643982.

(JOSL-) JOSLIN DIABETES CENT INC.

Kahn CR, White MF, Rothenberg PL;

MPI: 1992-365881/44.

P-PSDB; AAR28047.

Purified nucleic acid encoding Insulin Receptor Substrate - used to
prepare IRS-1, for diagnosis and treatment of insulin related diseases
and abnormal cellular proliferation.

Disclosure; Fig 12; 128pp; English.

The sequence given encodes the rat insulin receptor substrate-1 (IRS-1).

The IRS-1 was isolated using the probe sequences given in AAQ29701-02.

The IRS-1 sequence can be inserted into a vector and used to transform
cells to produce IRS-1. The level of IRS-1 metabolism can then be studied
and abnormal levels may be seen to be indicative of insulin related
disease. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 5125 BP; 1185 A; 1479 C; 1358 G; 1103 T; 0 U; 0 Other;

3	GGATGAAGCTGACCCCCCCCCC		0;	Indels	0;	Gaps	0;
---	------------------------	--	----	--------	----	------	----

RESULT 27

AA568926;
XX

XX
XX

Human
diagnostic protein #4730.

WO200175067-A

11-OCT-2001.

31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00540217.

43-AUG-2000; 2000US-00649167.

Dimanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.
P-PSDB; ABG04739.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 4730; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probe, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. MA664197-MA694664 represent novel human diagnostic coding sequences of the invention. Note, the sequence data for this patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences

Very Match 28 T; 0 U; 0 Other

est Local Similarity 66.3%; Score 33.8; DB 5; Length 291
84.4%; Pred. No. 3;

[illegible]

RESULT 28

AC ABZ24593 ;
XX

[illegible]

Key

Key	Location/Qualifiers
FF	
TT	

156. .779
/*Caa= 3

07-NOV 2000

07-NOV-2002.

26-APR-2002; 2002WO-US013245

27-APR-2001; 2001US-00844864.

(BAYU) . BAYLOR COLLEGE MEDICINE
(AMHP) WYETH.

malczuk MM, Wang P, Bai Y, Wu X;

WPI; 2003-167110/16.
P-PSDB; ABP58237.

New ovary-specific genes comprising O1-180 or O1-236, useful for decreasing conception or enhancing fertility, or for the preparation of a composition for treating e.g. cancer.

Disclosure; Page 111-112, 141pp; English.

The present sequence is that of murine ovary-specific OI-236 cDNA. OI-236 is the mammalian orthologue of *Xenopus laevis* nucleoplasmin, and the OI-236 gene has been named Npm2 (see also AB224594). OI-236 cDNAs were initially identified by subtractive hybridisation using ovaries from knockout and wild-type mice. Full-length Npm2 cDNA (clone 236-1) was used to identify the mouse Npm2 gene in a genomic library; this gene maps to chromosome 14. Loss of Npm2 results in female infertility and sterility in mice and human OI-180, OI-184 and OI-236 polynucleotides and various cell proliferative or degenerative disorders, especially those involving ovarian tumours, such as germ line tumours and granulosa cell tumours, or infertility, such as premature ovarian failure. The invention provides a method for detection of a cell proliferative or degenerative disorder of the ovary, which is associated with the expression of OI-180, OI-184 or OI-236. It also provides a method for treating such disorders by using an agent which suppresses or enhances the respective activities of OI-180, OI-184 or OI-236, and a method of screening for compounds that interact and/or modulate the expression or activity of the ovary-specific agents. These compounds are possible contraceptive or fertility enhancing polynucleotide sequence

```
Query Match          66.3%; Score 33.8; DB 7; Length 1018;
Best Local Similarity 84.4%; Pred. No. 3.2;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      528 GAAGATGACGAGGAAGAGGAGGAGGAGGAGGAGGAGATGAA 572

RESULT 29
AAD00296
ID      AAD00296 standard; cDNA; 1019 BP.
XX
AC      AAD00296;
XX
DT      05-SEP-2000 (first entry)
XX
DE      Mouse oocyte-specific OI-236 cDNA clone.
XX
KM      Oocyte-specific; ovary; OI-236; mouse; Npm2; gynaecological; treatment;
KW      nucleoplasmic; cell proliferative disorder; cell degenerative disorder;
KW      contraceptive; ovulation; signalling pathway; human infertility; cancer;
KW      screen; modulator; ss.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      CDS      156..779
                /tag= a
                /product= "Mouse oocyte-specific protein, OI-236"
                /note= "identical to mouse Npm2 protein with the
                exception of one residue"
FT
FT
FT
PN      WO200024755-A1.
XX
PD      04-MAY-2000.
XX
PF      28-OCT-1999; 99WO-US025209.
XX
PR      28-OCT-1998; 98US-0106020P.
XX
PA      (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI      Matzuk MM, Wang P;
XX
DR      WPI; 2000-350684/30.
XX
P-PSDB; AAY70950.
XX
PT      OI-180, OI-184 and OI-236 polypeptides and nucleic acids encoding them,
PT      useful for evaluating potential contraceptives to block ovulation in a
PT      reversible manner.
XX
PS      Claim 22; Fig 5; 54pp; English.
XX
CC      The present sequence is the mouse oocyte-specific gene Npm2, complete
CC      cDNA clone OI-236. It is derived from mouse 2-cell embryo cDNA library
CC      and expressed in the oocytes of intermediate size type 3a follicles and
CC      all type 3b follicles. This clone is used to screen and identify the
CC      mouse Npm2 gene. It is homologous to Xenopus laevis nucleoplasmic (Xnm2)
CC      expressed exclusively in eggs. It provides in vitro and in vivo reagents
CC      for studying ovarian development and function. This sequence has
CC      gynaecological and contraceptive activity. Agents which modulate OI-180,
CC      OI-184 and OI-236 may be used to treat cell proliferative or degenerative
CC      disorders, associated with abnormal expression of these ovary specific
CC      genes. This ovary-specific sequence can be used as reagents to evaluate
CC      potential contraceptives, to block ovulation in a reversible manner. It
CC      is also used to screen for genetic mutations in signalling pathways, that
CC      are associated with some forms of human infertility or gynaecological
CC      cancers
XX
SO      Sequence 1019 BP; 334 A; 243 C; 265 G; 177 T; 0 U; 0 Other;
```

```
Query Match          66.3%; Score 33.8; DB 3; Length 1019;
Best Local Similarity 84.4%; Pred. No. 3.2;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      528 GAAGATGACGAGGAAGAGGAGGAGGAGGAGGAGGAGATGAA 572

RESULT 30
AAD00297
ID      AAD00297 standard; DNA; 1481 BP.
XX
AC      AAD00297;
XX
DT      05-SEP-2000 (first entry)
XX
DE      Mouse ovary-specific Npm2 gene.
XX
KM      Oocyte-specific; ovary; Npm2; nucleoplasmic; mouse; mammalian ortholog;
KW      chromosome 14; human chromosome 8p21; contraceptive; gynaecology; cancer;
KW      cell proliferative disorder; cell degenerative disorder; ovulation;
KW      modulator; human infertility; signalling pathway; screen; treatment; ds.
XX
OS      Mus sp.
XX
FH      Key      Location/Qualifiers
FT      5'UTR     1..150
                /tag= a
FT      exon      151..199
                /tag= b
FT      intron     200..230
                /tag= c
                /number= 1
FT      misc_feature 215
                /tag= d
                /note= "Corresponds to 314 missing nucleotides of intron
                1 between bases 214 and 216"
FT      exon      231..394
                /tag= e
                /number= 2
FT      CDS        337..1177
                /tag= f
                /product= "Mouse ovary-specific Npm2 protein"
                /note= "Coding region is interrupted by 8 introns"
FT      intron     395..425
                /tag= g
                /number= 2
FT      misc_feature 410
                /tag= h
                /note= "Corresponds to 105 missing nucleotides of intron
                2 between bases 409 and 411"
FT      exon      426..511
                /tag= i
                /number= 3
FT      misc_feature 473
                /tag= j
                /note= "The 'T' is replaced with 'G' in the cDNA"
FT      intron     512..542
                /tag= k
                /number= 3
FT      misc_feature 527
                /tag= l
                /note= "Corresponds to 63 missing nucleotides of intron 3
                between bases 526 and 528"
FT      exon      543..656
                /tag= m
                /number= 4
FT      intron     657..687
                /tag= n
                /number= 4
FT      misc_feature 672
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PS Example 5; Fig 13; 54pp; English.

CC The present sequence is the mouse ovary-specific Npm2 gene, mapped to the
CC middle of mouse chromosome 14. It shows linkage to D1Mit32, this region
CC being syntenic to human chromosome 8p21. The clone O1-236 cDNA is used to
CC screen and identify Npm2 gene. It is the mammalian ortholog of Xenopus
CC laevis nucleoplasmin (Npm2) expressed exclusively in the eggs. It
CC provides in vitro and in vivo reagents for studying ovarian development
CC and function. This sequence has gynaecological and contraceptive
CC activity. Agents which modulate O1-180, O1-184 and O1-236 may be used to
CC treat cell proliferative or degenerative disorders, associated with
CC abnormal expression of these ovary specific genes, this ovary-specific
CC sequence can be used as reagents to evaluate potential contraceptive
CC genetic mutations in a reversible manner. It is also used to screen for
CC genetic mutations in signalling pathway, that is associated with some
CC form of human infertility or gynaecological cancer

QX Sequence 1481 BP; 407 A; 379 C; 391 G; 296 T; 0 U; 8 Other;

QY Query Match 66.3%; Score 33.8; DB 3; Length 1481;
Best Local Similarity 84.4%; Fred. No. 3.3;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

DB 1 GAGGATGAACCTGAAGAGAGAGAGAGAGAGAGAGAGAGATGCGAA 45
833 GAAAGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAA 877

Search completed: February 29, 2004, 20:36:16
Job time : 275 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 14:57:29 ; Search time 2149 Seconds
(without alignments)
708.688 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930

Perfect score: 51

Sequence: 1 gagagctgaagctggaagagga.....aggaagagctggaaccacag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database :
1: EST:*
2: em_estba:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_ges_hum:*
18: em_ges_inv:*
19: em_ges_pln:*
20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rtd:*
26: em_ges_phg:*
27: em_ges_vrt1:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.6	81.6	1353	29	AY416856 Homo sapi
2	40	78.4	1044	13	BQ880026 AGENCOURT
3	38.8	76.1	1347	29	AY416858 Mus muscu
4	38.2	74.9	872	29	ECMA2BAR AL606560 Horse alp

C	5	37.8	74.1	633	9	AL872808	AL872808
C	6	37.8	74.1	634	9	AL852740	AL852740
C	7	37	72.5	642	14	CF360731	CF360731
C	8	37	72.5	787	13	BU748295	BU748295
C	9	36.4	71.0	770	28	B2195097	B2195097
C	10	36.2	71.0	256	14	CA315228	CA315228
C	11	36	70.6	490	9	AA896321	AA896321
C	12	36	70.6	763	14	CB625989	CB625989
C	13	36	70.6	822	12	CB625990	CB625990
C	14	35.4	69.4	362	12	BM659898	BM659898
C	15	35.4	69.4	378	13	BQ294503	BQ294503
C	16	35.4	69.4	399	12	BI961415	BI961415
C	17	35.4	69.4	446	12	BI961033	BI961033
C	18	35.4	69.4	447	9	AL842491	AL842491
C	19	35.4	69.4	446	10	AW760136	AW760136
C	20	35.4	69.4	512	14	CB272922	CB272922
C	21	35.4	69.4	552	14	CF795982	CF795982
C	22	35.4	69.4	556	13	BX669429	BX669429
C	23	35.4	69.4	571	13	BX676418	BX676418
C	24	35.4	69.4	586	9	AI451753	AI451753
C	25	35.4	69.4	608	14	CF367914	CF367914
C	26	35.4	69.4	673	14	CF792336	CF792336
C	27	35.4	69.4	677	13	BY706040	BY706040
C	28	35.4	69.4	823	28	BZ504700	BZ504700
C	29	35.4	69.4	1080	11	AK005900	AK005900
C	30	35.4	69.4	1595	11	AK008242	AK008242
C	31	35	68.6	304	14	CA618111	CA618111
C	32	35	68.6	528	28	AZ993348	AZ993348
C	33	35	68.6	627	10	BF220068	BF220068
C	34	35	68.6	617	10	AW388194	AW388194
C	35	35	68.2	1009	29	CNS04V62	CNS04V62
C	36	34.8	68.2	464	9	AL791191	AL791191
C	37	34.8	68.2	648	9	AL652867	AL652867
C	38	34.8	68.2	649	9	AL848797	AL848797
C	39	34.8	68.2	861	13	BX736262	BX736262
C	40	34.8	68.2	891	13	BX694066	BX694066
C	41	34.8	68.2	895	13	BX771143	BX771143
C	42	34.8	68.2	899	9	AL970754	AL970754
C	43	34.6	67.8	354	14	CB961043	CB961043
C	44	34.6	67.8	411	14	CD565314	CD565314
C	45	34.6	67.8	516	14	CA567661	CA567661
C	46	34.6	67.8	527	14	BE303747	BE303747
C	47	34.6	67.8	528	9	AA516854	AA516854
C	48	34.6	67.8	560	14	CD544688	CD544688
C	49	34.6	67.8	566	10	BE573037	BE573037
C	50	34.6	67.8	592	14	CF909740	CF909740
C	51	34.6	67.8	598	13	BQ550624	BQ550624
C	52	34.6	67.8	611	14	CA877352	CA877352
C	53	34.6	67.8	618	14	CF908392	CF908392
C	54	34.6	67.8	664	14	CF540205	CF540205
C	55	34.6	67.8	676	14	CB527359	CB527359
C	56	34.6	67.8	689	12	BG871040	BG871040
C	57	34.6	67.8	698	13	BQ769050	BQ769050
C	58	34.6	67.8	706	12	BM963803	BM963803
C	59	34.6	67.8	741	10	BE916440	BE916440
C	60	34.6	67.8	767	12	BI151285	BI151285
C	61	34.6	67.8	889	13	BQ933453	BQ933453
C	62	34.6	67.8	912	13	BQ885027	BQ885027
C	63	34.6	67.8	919	14	AK004698	AK004698
C	64	34.6	67.8	2755	11	CF732419	CF732419
C	65	34.4	67.5	394	14	CF32419	CF32419
C	66	34.4	67.5	478	14	CB731230	CB731230
C	67	34.4	67.5	497	9	AU066373	AU066373
C	68	34.4	67.5	498	10	BF441671	BF441671
C	69	34.4	67.5	537	10	BF077495	BF077495
C	70	34.4	67.5	773	14	CA817872	CA817872
C	71	34.4	67.5	780	12	BI695609	BI695609
C	72	34.4	67.5	804	28	BZ236037	BZ236037
C	73	34.4	67.5	914	14	CF212881	CF212881
C	74	34.4	67.5	1027	12	BM476983	BM476983
C	75	34.4	67.5	1201	9	AL524694	AL524694
C	76	34.2	67.1	501	28	AZ269523	AZ269523
C	77	34.2	67.1	846	29	CNS04HSP	CNS04HSP

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt BioScience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM13559 row: 1 column: 20
High quality sequence stop: 430.

FEATURES

source

1..1044

Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6179035"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupeki dorsal root ganglion"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
Noti; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCG-3' and
5'-GACTAGTCTAGTCGCGAGCGCCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupeki, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Query Match 78.4%; Score 40; DB 13; Length 1044;
Best Local Similarity 98.1%; Pred. No. 23;
Matches 51; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAGGATGAACTGTAAGA-GGAGGAGGAGGAGGAGGAGTGTGAACCCAG 51
|||||
Db 417 GAGGATGAACTGTAAGAAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCAG 466

RESULT 3
LOCUS AY416858 1347 bp DNA linear GSS 12-DEC-2003
DEFINITION Mus musculus HCM6030 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416858
VERSION AY416858.1 GI:39772818
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 1347)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Perliera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1347)
AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Perliera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Direct Submission

COMMENT Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

source

1..1347

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM6030"

ORIGIN

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Best Local Similarity 86.0%; Pred. No. 43;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAGGATGAACTGTAAGAAGGAGGAGGAGGAGGAGTGTGAACCCCA 50
|||||
Db 883 GAGGATGAACTGTAAGAAGGAGGAGGAGGAGGAGTGTGAACCCCA 932

RESULT 4
LOCUS ECMA2BAR 872 bp DNA linear GSS 14-SEP-2001
DEFINITION Horse alpha2 adrenergic receptor gene fragment probably subtype b,
genomic survey sequence.

ACCESSION AL606560
VERSION AL606560.1 GI:15591917
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE Equus caballus (horse)
ORGANISM Equus caballus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
AUTHORS 1 (bases 1 to 872)
Hunter, C. and Elgar, G.

TITLE Alpha2 adrenergic receptor gene
REFERENCE 2 (bases 1 to 872)
AUTHORS Hunter, C.
JOURNAL Direct Submission

Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biocelphgmp.mrc.ac.uk

FEATURES

source

1..872

Location/Qualifiers

/organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"

ORIGIN

Query Match 74.9%; Score 38.2; DB 29; Length 872;
Best Local Similarity 84.3%; Pred. No. 55;
Matches 43; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAGGATGAACTGTAAGAAGGAGGAGGAGGAGGAGTGTGAACCCAG 51
|||||
Db 592 GAGGATGAACTGTAAGAAGGAGGAGGAGGAGGAGGAGTGTGAACCCAG 642

RESULT 5
LOCUS AL872808 633 bp mRNA linear EST 03-DEC-2003
DEFINITION AL872808 KXC-egg Silurana tropicalis cDNA clone TEG106K18 5', mRNA
sequence.

ACCESSION AL872808
VERSION AL872808.2 GI:38666205
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Silurana.

TITLE 1 (bases 1 to 633)
AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22893073.

COMMENT Contact: Taylor R

LOCUS	BU748295	787 bp	mRNA	linear	EST 10-OCT-2002
DEFINITION	CH3#019_B01T7 Canine heart heart normalized cDNA library in pBluescript				
ACCESSION	Canis familiaris cDNA clone CH3#019_B01 5', mRNA sequence.				
VERSION	BU748295.1	GI:23700479			
KEYWORDS	EST.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
AUTHORS	1 (bases 1 to 787)				
TITLE	Yi, Y., Desai, R., Larte, M., Henthorn, P. and George A.L.				
JOURNAL	Expressed sequence tags from Canine heart				
COMMENT	Unpublished (2003)				
	Other_ESTs: CH3#019_B01T3				
	Contact: George A.L.				
	Division of Genetic Medicine				
	Vanderbilt University				
	529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA				
	Tel.: 615 936 2660				
	Fax: 615 936 2661				
	Email: a1.george@vanderbilt.edu				
	Insert Length: 1072 Std Error: 0.00				
	Seq primer: T7: TAATACGACCTCATATAGCG				
	High quality sequence start: 41				
	High quality sequence stop: 785.				
	Location/Qualifiers				
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source	/organism="Canis familiaris"				
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	/cell_type="heart"				
	/dev_stage="mixed developmental stages (adult, 30 day - 40 day Fetal)"				
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	/note="Organ: heart; Vector: pBluescript; Site: 1: 5' of vector NotI; Site: 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dt primed"				
ORIGIN					
Query Match	72.5%	Score 37;	DB 13;	Length 787;	
Best Local Similarity	86.9%	Pred. No. 99;			
Matches	40;	Conservative	0;	Mismatches	5; Indels 0; Gaps 0;
Qy	1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGATGTGAA	45			
Db	41 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAA	85			
RESULT 9	B2195097	770 bp	DNA	linear	GSS 11-OCT-2002
LOCUS	CH230-248B14.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone				
DEFINITION	CH230-248B14, genomic survey sequence.				
ACCESSION	B2195097				
VERSION	B2195097.1	GI:23853149			
KEYWORDS	GSS.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
	1 (bases 1 to 770)				
	Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Ruggie, P., de Jong, P. and Fraser, C.M.				
	Rat BAC end sequences from Library CHORI-230 MboI segment				
TITLE					

[illegible]

Matches	39;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA	44						
Db	601	GAGGAAGAAGAAGAGAGGAGGAGGAGGAGGAAGAAGAGCGA	644						
RESULT 13									
LOCUS	CB625990/c	822 bp	mRNA	linear	EST 08-APR-2003				
DEFINITION	clone OS1Ea15013.r OS1Ea Oryza sativa (indica cultivar-group) cDNA								
ACCESSION	CB625990								
VERSION	CB625990.1	GI:29620979							
KEYWORDS	EST.								
SOURCE	Oryza sativa (indica cultivar-group)								
ORGANISM	Oryza sativa (indica cultivar-group)								
REFERENCE	Oryza sativa (indica cultivar-group)								
AUTHORS	Eubaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.								
TITLE	1 (bases 1 to 822)								
JOURNAL	Jantaeurayrat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,...								
COMMENT	Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G. Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea Unpublished (2003) Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210089, Tucson, AZ 85721-0089, USA Tel: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu PCR Primers FORWARD: gta aaa cga cgg cca gtc BACKWARD: gga aac agc tat gac cat g Plate: 15 row: 0 column: 13 Seq primer: gga aac agc tat gac cat g. Location/Qualifiers 1..822 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="IR36" /db_xref="taxon:39946" /clone="OS1Ea15013" /tissue_type="leaf" /dev_stage="3 week" /lab_host="DH10B" /clone_1fb="OS1Ea" /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Lesion M1mC SPL 11"								
FEATURES	source								
ORIGIN									
Query Match	70.6%;	Score 36;	DB 14;	Length 822;					
Best Local Similarity	88.6%;	Pred. No. 1.7e+02;							
Matches	39;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
Qy	1	GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA	44						
Db	594	GAGGAAGAAGAAGAGAGGAGGAGGAGGAAGAAGAGCGA	551						
RESULT 14									
LOCUS	BM659898/c	365 bp	mRNA	linear	EST 27-FEB-2002				
DEFINITION	BUB602768846.R1 CSEQFXJ38 pig thyroid and parathyroid Sus scrofa								
ACCESSION	BM659898								
VERSION	BM659898.1	GI:18962904							
KEYWORDS	EST.								
SOURCE	Sus scrofa (pig)								
ORGANISM	Sus scrofa								

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Cetartiodactyla: Suidae, Sus.
AUTHORS 1 (bases 1 to 365)
TITLE Adelson, D.L. and Gill, C.A.
JOURNAL Porcine ESTs
COMMENT Unpublished (2002)
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
1. 365
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/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="CSEBPX13 pig thyroid and parathyroid"
/note="Organ: thyroid and parathyroid gland; Vector:
pBluescript SK+; Site 1: NotI; Site 2: EcoRI; sequence 5'
of the insert (5'-NNN...NNN(insert)
GCGATTCGAGCTCCACCGCGTGGCGCGCGCGTGGAG. sequence 3' of
the inserts (AAGATTCGATTCATCACTTATCATCATCGTCGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."

ORIGIN
Query Match 69.4%; Score 35.4; DB 12; Length 365;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 149 GAGAGGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
|||||
GAGAGGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGTGTGAA 105

RESULT 15 378 bp mRNA linear EST 15-MAY-2002
BQ294503
LOCUS BQ294503
DEFINITION americana cDNA clone 5, mRNA sequence.
ACCESSION BQ294503
VERSION BQ294503.1 GI:20803437
KEYWORDS EST.
SOURCE Periplaneta americana (American cockroach)
ORGANISM Periplaneta americana
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
Blattellidae; Periplaneta.
1 (bases 1 to 378)
Zhou, Z.W., Liu, Z.G. and Gao, B.
The construction of Periplaneta americana nymph cDNA library and
IgG4 immunology screen
Unpublished (2002)
Contact: Zhou, Z.W.
Immunology Department
Jiang Xi Medical College
106, Bayi Street, Nanchang, Jiangxi, P.R.C.
Tel: 86-0791-6363001
Email: Zhouzhenwen28@hotmail.com.
Location/Qualifiers
1. 378
/organism="Periplaneta americana"
/mol_type="mRNA"
/db_xref="taxon:6978"
/clone="5"
/issue_type="whole body"
/dev_stage="nymph"
/lab_host="E.coli NM522"
/clone_lib="periplaneta americana Lambda Express library"
/note="Vector: Lambda Excell; These sequences were
screened by cockroach sensitive patients' IgG4 serum "

FEATURES
source

Kiyoshi Kikuchi, Shugo Matabe
Laboratory of Aquatic Molecular Biology and Biotechnology, Graduate
School of Agricultural and Life Sciences, The University of Tokyo,
Bunkyo-ku, Tokyo 108-6639, Japan
Library sequenced by Melody S. Clark and Amanda Thompson MRC Human
Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10
1SB, UK.

Location/Qualifiers
1. .447

Query Match	69.4%	Score 35.4;	DB 9;	Length 447;
Best Local Similarity	86.7%	Pred. No. 2e+02;		
Matches 39;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0

RESULT 19
AM760336

DEFINITION
s149606.y1 Gm-cl027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID
Gm-cl027-4619 5' similar to TR:O82214 O82214 T29E15.4 PROTEIN. ;,
mRNA sequence.

TITLE	Public Soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R/Public Soybean EST Project

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cd@resgen.com
Insert Length: 1134 Std Error: 0.00
High quality sequence stop: 424.

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Location/Qualifiers
1. 496
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
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clone_11b="Gm-cl021"

/note=Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (TAA, C, or G) was added to the 3' end of the primer (GGAGAGGAGAGAGAGAGAACTTCTCGAG(T)18) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript (cm) II XR predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia Corryell."

Query Match:	69.4%	Score 35.4;	DB 10;	Length 496;
Best Local Similarity	84.8%	Pred. No. 2.1e+02;		
Matches 39;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0

Oy 1 GAGATGAAGCTGAAAGAGAAGAGAGAGAAGTGTGAAC 46
 ||||| | | | | | | | | | | | | | | | | |
Db 365 GAGATGAGGATGATGAGAGAGAAGAGAGCGATTGTNTGACC 410

RESULT 20	512 bp	linear	EST 24-FEB-2007
CB272922/c			
LOCUS			
DEFINITION			
IMAGE:6446341 5', mRNA sequence.			
CA072922			
ma64407.y1			
McGarrey Eddy			
spermatocytes			
Mus musculus			
CDNA clone			

ORGANISM Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 512)
REFERENCE McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Page, D.,
Martin, J., Wylie, T., Dante, M., Bowers, Y., Thelsting, B., Gibbons, M.,
Ritter, E., Tsagarashvili, R., Ronko, I., Maguire, L., Kennedy, S.,
Bennett, D., Watson, R. and Wilson, R.
TITLE NIH3 Mouse
JOURNAL
COMMENT
Unpublished (2002)
Contact: McCarrey/Eddy NIH3 Mouse

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu

Query Match 69.4%; Score 35.4; DB 13; Length 556;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
|||||
394 GAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 438

RESULT 23
BX676418 571 bp mRNA linear EST 28-OCT-2003
LOCUS BX676418 Sus scrofa library (scac) Sus scrofa cDNA clone
DEFINITION scac00311.e.12 3prtm, mRNA sequence.
ACCESSION BX676418
VERSION BX676418.1 GI:38010553
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 571)
Bonnef, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldi, F. and Haley, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@clouise.inra.fr
Clone distribution: AGENAE Resource centre, Francois PUMI,
Francois.Plum@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
genome (LRBG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
FRANCE. +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptor and repetitions. Contact us
at bigenashport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0031, row: e column: 12.
Location/Qualifiers
1..571
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00311.e.12"
/tissue_type="mixed"
/clone_lib="Sus scrofa library (scac)"
/note="Vector: pT73D-pac vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN
Query Match 69.4%; Score 35.4; DB 13; Length 571;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
|||||
395 GAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 439

RESULT 24
A1451753 586 bp mRNA linear EST 15-MAR-2000
LOCUS A1451753/c
DEFINITION mb16f09.y1 Soares mouse p3NMFI9.5 Mus musculus cDNA clone
IMAGE:329609 5' similar to TR:Q12804 Q12804 RECEPTIN.;, mRNA

sequence.
ACCESSION A1451753
VERSION A1451753.1 GI:4306203
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 586)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,
Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
MG1:211009
Seq primer: -40RP from Gibco
High quality sequence scop: 457
POLYA=No.
Location/Qualifiers
1..586
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:329609"
/dev_stage="19.5 dpc total fetus"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares mouse p3NMFI9.5"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer (5',
TGTTACCATCTGAGTGGAGCGCGCATTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldi. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

ORIGIN
Query Match 69.4%; Score 35.4; DB 9; Length 586;
Best Local Similarity 86.7%; Pred. No. 2.1e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
|||||
227 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 183

RESULT 25
CF367914 608 bp mRNA linear EST 25-AUG-2003
LOCUS CF367914/c
DEFINITION 852497 MARC 3P1G Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CF367914
VERSION CF367914.1 GI:34172915
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

ORIGIN

Oy 1 GAGGATGAAGCTGAAGAAGAGAGAGAGAGAAAGACTGTGAA 45
 |||||
Db 448 GAGGAGGAAGAGAAAGAGAGAGAGAGAGAGAAAGAGAGAA 407
 |||||

FEATURES

ORIGIN

OY 1 GAGGATGAAGCTGAAGAAGCAGCAGCAGGAGGAAAGTGTCAA 45
 |||||
Db 40 GAGGAGGAGATGAAGAAGCAGCAGCAGGAGGAGGAGCAGCA 84

.. PUMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS

JOURNAL
MEDLINE
PUBMED
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

TITLE	ABSTRACT	KEYWORDS	URL
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			

COMMENT Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp,
URL:http://genome.gs.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gs.riken.go.jp/) for
further details.

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGAGATCCAGAGACTCTTTTCTTTTCTTNN 3'], cDNA was
prepared by using trihalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0 and subtraction to
Rot = 20.0. Second strand cDNA was prepared with the primer adapter
of sequence[5'
GAGAGAGAGATTCGAGTTAATTAAATTATCCCCCCCCC 3']. cDNA was cleaved
with XhoI and ScaI. Cloning sites, 5' end: XhoI; 3' end: ScaI.
Host: SOLR.

FEATURES

source

location/Qualifiers

1..1595
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:2010015A19"
/db_xref="MGI:189821"
/db_xref="taxon:10090"
/clone="2010015A19"
/sex="male"
/issue_type="small intestine"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1..1595
/note="similar to CBP1 INTERACTING COREPRESSOR CIR [Homo
sapiens] (SPTRI095367, evidence: FASTV, 77.6%ID,
96.4%length, match=1347)"

ORIGIN

misc_feature

Query Match 69.4%; Score 35.4; DB 11; Length 1595;
Best Local Similarity 86.7%; Pred.No.2.5e+02;

Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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|||||
DB 922 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 878
|||||

Search completed: February 29, 2004, 21:48:25
Job time : 2171 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: February 29, 2004, 20:27:29 ; Search time 62.5 Seconds
(without alignments)
452,840 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930

Perfect score: 51
Sequence: 1 gagcgatgaagcgcgaagagga.....agggaagcgtgaacccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A COMB. seq:*
- 2: /cgn2_6/prodata/2/ina/5B COMB. seq:*
- 3: /cgn2_6/prodata/2/ina/6A COMB. seq:*
- 4: /cgn2_6/prodata/2/ina/6B COMB. seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS COMB. seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	41.6	81.6	2072	4 US-09-016-434-1181	Sequence 1181, Ap
2	36.6	71.8	593	4 US-09-691-538A-12	Sequence 12, Appl
3	35	68.6	1820	5 PCT-US94-09752-1	Sequence 1, Appl
4	34.2	67.1	5125	1 US-08-094-948A-4	Sequence 4, Appl
5	34.2	67.1	5125	5 PCT-US96-09319-4	Sequence 4, Appl
6	33	64.7	650	3 US-09-328-111-333	Sequence 333, App
7	32.8	64.3	404	4 US-09-621-976-18769	Sequence 18769, A
8	32.6	63.9	661	4 US-09-694-998A-34	Sequence 34, Appl
9	32.2	63.1	2817	4 US-09-620-312D-1085	Sequence 1085, Ap
10	32.2	63.1	14561	4 US-09-392-714-1	Sequence 1, Appl
11	31.8	62.4	636	4 US-09-702-705-1668	Sequence 1668, Ap
12	31.8	62.4	636	4 US-09-736-457-1668	Sequence 1668, Ap
13	31.8	62.4	636	4 US-09-614-124B-1668	Sequence 1668, Ap
14	31.8	62.4	636	4 US-09-671-125-1668	Sequence 1668, Ap
15	31.6	62.0	258	4 US-09-345-882-21	Sequence 21, Appl
16	31.6	62.0	3211	2 US-08-574-859A-8	Sequence 8, Appl
17	31.6	62.0	3211	3 US-09-357-014-8	Sequence 8, Appl
18	31.6	62.0	3901	2 US-08-574-859A-6	Sequence 6, Appl
19	31.6	62.0	3901	3 US-09-357-014-6	Sequence 6, Appl
20	31.6	62.0	4226	4 US-09-620-312D-480	Sequence 480, App
21	31.6	62.0	6002	4 US-09-345-882-4	Sequence 4, Appl
22	31.6	62.0	162450	4 US-09-345-882-1	Sequence 1, Appl
23	31.4	61.6	2556	4 US-09-817-510-1	Sequence 1, Appl
24	31.2	61.2	129	4 US-09-702-705-309	Sequence 309, App
25	31.2	61.2	129	4 US-09-736-457-309	Sequence 309, App
26	31.2	61.2	129	4 US-09-614-124B-309	Sequence 309, App
27	31.2	61.2	129	4 US-09-671-125-309	Sequence 309, App

28	31.2	61.2	129	4 US-09-589-184-309	Sequence 309, App
29	31.2	61.2	403	4 US-09-621-976-18731	Sequence 18731, A
30	31.2	61.2	427	4 US-09-621-976-18711	Sequence 18711, A
31	31.2	61.2	438	4 US-09-702-705-1028	Sequence 1028, Ap
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35	31.2	61.2	450	4 US-09-621-976-3667	Sequence 3667, Ap
36	31.2	61.2	452	4 US-09-621-976-3669	Sequence 3669, Ap
37	31.2	61.2	458	4 US-09-621-976-1227	Sequence 1227, Ap
38	31.2	61.2	459	4 US-09-621-976-1224	Sequence 1224, Ap
39	31.2	61.2	464	4 US-09-621-976-1223	Sequence 1223, Ap
40	31.2	61.2	464	4 US-09-621-976-3665	Sequence 3665, Ap
41	31.2	61.2	464	4 US-09-621-976-18704	Sequence 18704, A
42	31.2	61.2	476	4 US-09-621-976-18704	Sequence 18704, A
43	31.2	61.2	514	4 US-09-621-976-3661	Sequence 3661, Ap
44	31.2	61.2	521	4 US-09-621-976-18772	Sequence 18772, A
45	31.2	61.2	686	4 US-09-166-350-9	Sequence 166, Ap
46	31.2	61.2	1147	4 US-09-016-434-1251	Sequence 1251, Ap
47	31.2	61.2	1275	1 US-08-552-142A-3	Sequence 3, Appl
48	31.2	61.2	1275	1 US-08-910-973-3	Sequence 3, Appl
49	31.2	61.2	1275	1 US-09-499-227-3	Sequence 3, Appl
50	31.2	61.2	1275	5 PCT-US95-05741-3	Sequence 3, Appl
51	31.2	61.2	2663	4 US-09-533-029-47	Sequence 47, Appl
52	31.2	61.2	2663	4 US-09-533-029-47	Sequence 47, Appl
53	31.2	61.2	5561	4 US-09-418-710-28	Sequence 28, Appl
54	31.2	61.2	5573	4 US-09-418-710-30	Sequence 30, Appl
55	31	60.8	675	1 US-07-807-043B-2	Sequence 2, Appl
56	31	60.8	675	1 US-08-299-849B-4	Sequence 2, Appl
57	31	60.8	675	2 US-08-142-368A-2	Sequence 2, Appl
58	31	60.8	675	3 US-08-967-727-2	Sequence 2, Appl
59	31	60.8	675	3 US-08-037-230D-2	Sequence 2, Appl
60	31	60.8	675	4 US-09-583-850-2	Sequence 2, Appl
61	31	60.8	675	4 US-09-579-197-2	Sequence 2, Appl
62	31	60.8	675	4 US-09-404-026-2	Sequence 2, Appl
63	31	60.8	675	4 US-09-312-464-2	Sequence 2, Appl
64	31	60.8	1365	1 US-07-807-043B-4	Sequence 4, Appl
65	31	60.8	1365	1 US-08-299-849B-4	Sequence 4, Appl
66	31	60.8	1365	2 US-08-142-368A-4	Sequence 4, Appl
67	31	60.8	1365	3 US-08-967-727-4	Sequence 4, Appl
68	31	60.8	1365	3 US-08-037-230D-4	Sequence 4, Appl
69	31	60.8	1365	4 US-09-583-850-4	Sequence 4, Appl
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73	31	60.8	2184	3 US-08-955-918C-1	Sequence 1, Appl
74	31	60.8	2184	4 US-08-697-766A-1	Sequence 1, Appl
75	31	60.8	2518	3 US-09-433-699-3	Sequence 3, Appl
76	31	60.8	4698	1 US-07-807-043B-5	Sequence 5, Appl
77	31	60.8	4698	1 US-08-299-849B-5	Sequence 5, Appl
78	31	60.8	4698	2 US-08-142-368A-5	Sequence 5, Appl
79	31	60.8	4698	3 US-08-967-727-5	Sequence 5, Appl
80	31	60.8	4698	3 US-08-037-230D-5	Sequence 5, Appl
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82	31	60.8	4698	4 US-09-579-197-5	Sequence 5, Appl
83	31	60.8	4698	4 US-09-404-026-5	Sequence 5, Appl
84	31	60.8	4698	4 US-09-312-464-5	Sequence 5, Appl
85	31	60.8	6114	4 US-09-495-716A-5	Sequence 5, Appl
86	30.8	60.4	1194	4 US-09-220-132-31	Sequence 31, Appl
87	30.8	60.4	2120	4 US-09-149-476-160	Sequence 160, App
88	30.8	60.4	2277	4 US-09-310-463-3	Sequence 3, Appl
89	30.8	60.4	2277	4 US-08-842-248A-3	Sequence 3, Appl
90	30.8	60.4	2790	4 US-08-985-950-21	Sequence 21, Appl
91	30.8	60.4	2790	4 US-09-406-049-21	Sequence 21, Appl
92	30.8	60.4	2922	4 US-09-310-463-1	Sequence 1, Appl
93	30.8	60.4	2922	4 US-08-842-248A-1	Sequence 1, Appl
94	30.6	60.0	58	3 US-08-860-023-16	Sequence 16, Appl
95	30.6	60.0	1954	4 US-09-580-923-16	Sequence 16, Appl
96	30.6	60.0	1954	4 US-08-997-829-3	Sequence 3, Appl
97	30.6	60.0	1954	1 US-08-577-403-3	Sequence 3, Appl
98	30.6	60.0	2520	4 US-09-023-655-917	Sequence 917, App
99	30.6	60.0	2581	4 US-09-370-838-66	Sequence 66, Appl
100	30.6	60.0	3164	4 US-09-023-655-816	Sequence 816, App

[illegible]

COMPUTER READABLE FORM:

US-09-016-434-1181

Matches 44; C

1504 GAAAG

US-09-691-538A-12

Matches 42;

22 295 GAG

RESULT 3

```

PCT-US94-09752-1
Sequence 1, Application PC/TUS9409752
GENERAL INFORMATION:
APPLICANT: David S. Strayer and Avinash Chander
TITLE OF INVENTION: Compositions and Methods for
NUMBER OF INVENTIONS: Targeting Cells and Modulating Pulmonary Surfactant Secretion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09752
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/176,218
FILING DATE: December 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/114,951
FILING DATE: August 31, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JEFF-0042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1820
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
PCT-US94-09752-1
Query Match 68.6%; Score 35; DB 5; Length 1820;
Best Local Similarity 88.4%; Pred. No. 0.1;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTG 43
Db 572 GAAGATGATGATGAAGAGGAGGAGGAGGAGGAGGAAGAAATGTG 614
RESULT 4
US-08-094-948A-4
Sequence 4, Application US/08094948A
Patent No. 5621075
GENERAL INFORMATION:
APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahnive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

```

1 COMPUTER: IBM PC Compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 SOFTWARE: Patentn Release #1.0, Version #1.25
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/08/094,948A
6 FILING DATE: 21-JULY-1993
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 07/643,982
9 FILING DATE: 18-JAN-1991
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Myers, Louis (PLM)
12 REGISTRATION NUMBER: 35,965
13 REFERENCE/DOCKET NUMBER: JDP-013DV
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (617)227-7400
16 TELEFAX: (617)227-5941
17
18 INFORMATION FOR SEQ ID NO: 4:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 5125 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: cDNA
25 FEATURE:
26 NAME/KEY: CDS
27 LOCATION: 589..4053
28 US-08-094-948A-4
29
30 Query Match 67.1%; Score 34.2; DB 1; Length 5125;
31 Best Local Similarity 83.0%; Pred. No. 0.19;
32 Matches 39; Conservative 0; Mismatches 8; Indels 0; Gaps 0.
33
34 Oy 3 GGATGAAGCTGTAAGAGGAGGAGGAGGAGGAGGAAGTGTGAACCCC 49
35 |||||
36 Db 53 GGAAGAGCGACAGAGAGGAGGAGGAGGAGGAAGAGGAGGAGGAACCCC 99
37
38 RESULT 5
39 PCT-US96-09319-4
40 Sequence 4, Application PC/TUS9609319
41 GENERAL INFORMATION:
42 APPLICANT: Kahn, C. Ronald
43 APPLICANT: White, Morris F.
44 APPLICANT: Rothenberg, Paul Louis
45 TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
46 NUMBER OF SEQUENCES: 29
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE: Lahive & Cockfield
49 STREET: 60 State Street, Suite 510
50 CITY: Boston
51 STATE: Massachusetts
52 COUNTRY: U.S.A.
53 ZIP: 02109
54
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 COMPUTER: IBM PC Compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: Patentn Release #1.0, Version #1.25
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: PCT/US96/09319
62 FILING DATE:
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: US 08/094,948
65 FILING DATE: 21-JULY-1993
66 APPLICATION NUMBER: US 07/643,982
67 FILING DATE: 18-JAN-1991
68 ATTORNEY/AGENT INFORMATION:
69 NAME: Myers, Louis (PLM)
70 REGISTRATION NUMBER: 35,965
71 REFERENCE/DOCKET NUMBER: JDP-013DV
72 TELECOMMUNICATION INFORMATION:
73 TELEPHONE: (617)227-7400
74 TELEFAX: (617)227-5941

```

Query Match	67.1%;	Score 34.2;	DB 5;	Length 5125;
Best Local Similarity	83.0%;	Pred. No. 0.19;		
Matches 39;	Conservative	0. Matched		

RESULT 6
US-09-328-111-333

Sequence 333, Application US/09328111
Patent No. 6262333

```

1  APPLICANT: Endege, Wilson O.
2  APPLICANT: Steinmann, Kathleen E.
3  APPLICANT: Astle, Jon H.
4  APPLICANT: Burgess, Christopher C.
5  APPLICANT: Bushnell, Steven E.
6  APPLICANT: Carroll III, Eddie
7  APPLICANT: Caltino, Theodore J.
8  APPLICANT: Dertl, Adnan
9  APPLICANT: Ford, Donna M.
10 APPLICANT: Lewis, Marcia E.
11 APPLICANT: Monahan, John E.
12 APPLICANT: Schlegel, Robert
13
14 TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
15 FILE REFERENCE: CCD-257 (US)
16
17 CURRENT APPLICATION NUMBER: US/09/328,111
18 CURRENT FILING DATE: 1999-06-08
19 EARLIER APPLICATION NUMBER: US 60/088,801
20 EARLIER FILING DATE: 1998-06-10
21
22 NUMBER OF SEQ ID NOS: 850
23
24 SOFTWARE: PastedQ for Windows Version 3.0
25
26 SEQ ID NO 333
27
28 LENGTH: 650
29
30 TYPE: DNA
31
32 ORGANISM: Homo sapiens
33
34 FEATURE:
35
36 NAME/KEY: misc_feature
37
38 LOCATION: (1)...(650)
39
40 OTHER INFORMATION: n = A,T,C or G
41
42 US-09-328-111-333

```

Query Match	64.7%;	Score 33;	DB 3;	Length 650
Best Local Similarity	79.6%;	Pred. No. 0.34;		
Matches 39;	Conservative	0.0;	Mismatches	10

[illegible]

RESULT 7
US-09-62

US-09-841-976-18769
Sequence 18769, Application US/09621976
Patent No. 663063
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Jobert, S.

```

? APPLICANT: Giordano, J.Y.
? TITLE OF INVENTION: ESTs and Encoded Human Proteins
? FILE REFERENCE: GENSET: 054PR2
? CURRENT APPLICATION NUMBER: US/09/621,976
? CURRENT FILING DATE: 2000-07-21
? NUMBER OF SEQ ID NOS: 19335
? SOFTWARE: patent.pm
? SEQ ID NO 18769
? LENGTH: 404
? TYPE: DNA
? ORGANISM: Homo sapiens
?
US-09-621-976-18769

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ORGANISM: Homo sapiens
US-09-621-976-18769

Query Match	64.3%	Score 32.8;	DB 4;	Length 404;
Best Local Similarity	84.1%;	Pred. No. 0.37;		
Matches 37;	Conservative 0;	Mismatches 7;	Indels	

1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 44
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 348 GAGGAGGAAGGTCGGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 391

RESULT 8

Sequence 34, Application US/09894998A
Patent No. 5537EE

```

1  APPLICANT: Hosken, Nancy Ann
2  APPLICANT: Craig H. Day
3  APPLICANT: Davin C. Dillon
4  APPLICANT: McGowan, Patrick
5  APPLICANT: Sleach, Paul R.
6  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
7  TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
8  FILE REFERENCE: 210121.538
9  CURRENT APPLICATION NUMBER: US/09/894A.998A
10 CURRENT FILING DATE: 2001-06-28
11 NUMBER OF SEQ ID NOS: 64
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 34
14 LENGTH: 661
15 TYPE: DNA
16 ORGANISM: HSV-2
17 US-09-894.998A-34

```

ORGANISM: HSV-2
US-09-894-998A-34

Query Match	63.9%	Score 32.6;	DB 4;	Length 661;
Best Local Similarity	89.7%	Pred. No. 0.44;		
Matches	35;	Conservative	0;	Mismatches 4.

QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAG 39
 |||||
 Db 42 GAGGAGGAGGCCGAAGAGGAGGAGGAGGAGCCGGAAGAG 4

RESULT 9
US-09-62

Sequence 1085, Application US/09620312D
Patent No. 6569662

```

? GENERAL INFORMATION:
? APPLICANT: Tang, Y. Tom
? APPLICANT: Liu, Chenghua
? APPLICANT: Asundi, Vinod
? APPLICANT: Zhang, Jie
? APPLICANT: Ren, Feiyan
? APPLICANT: Chen, Rui-hong
? APPLICANT: Zhao, Qing A.
? APPLICANT: Wehrman, Tom
? APPLICANT: Xue, Aidong J.
? APPLICANT: Yang, Yonghong
? APPLICANT: Wang, Jian-Rui
? APPLICANT: Zhou, Ping
? APPLICANT: Ma, Yungting
? APPLICANT: Wang, Dunrui

```


Db 2590 GAGGAGAAGAGAGAGAGATGAGAGAGAGA 2627

RESULT 17

US-09-357-014-8

Sequence 8, Application US/09357014

Patent No. 6291645

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi

and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/357,014

FILING DATE: 19-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/574,959

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: DFN-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 3211 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 439..3157

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-357-014-8

Query Match 62.0%; Score 31.6; DB 3; Length 3211;

Best Local Similarity 89.5%; Pred. No. 0.96;

Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGA 38

Db 2590 GAGGAGAAGAGAGAGAGATGAGAGAGAGA 2627

RESULT 18

US-08-574-959A-6

Sequence 6, Application US/08574959A

Patent No. 5962224

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi

and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/574,959A

FILING DATE: 19-Dec-95

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: DFN-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 3901 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 439..3847

US-08-574-959A-6

Query Match 62.0%; Score 31.6; DB 2; Length 3901;

Best Local Similarity 89.5%; Pred. No. 0.98; 4; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGA 38

Db 3280 GAGGAGAAGAGAGAGAGATGAGAGAGAGA 3317

RESULT 19

US-09-357-014-6

Sequence 6, Application US/09357014

Patent No. 6291645

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi

and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/357,014

FILING DATE: 19-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/574,959

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: DFN-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-357-014-6

Query Match 62.0%; Score 31.6; DB 3; Length 3901;
Best Local Similarity 89.5%; Pred. No. 0.98;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGA 38
DB 3280 GAGGAGAGAGAGAGAGAGAGAGATGAGAGAGAGAGA 3317

RESULT 20
US-09-620-312D-480
Sequence 480, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aneudi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yuning
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 480
LENGTH: 4226
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2982)
US-09-620-312D-480

Query Match 62.0%; Score 31.6; DB 4; Length 4226;
Best Local Similarity 89.5%; Pred. No. 0.99;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGA 38
DB 658 GATGAAGAGAGAGAGAGAGAGAGAGAGAGAGA 695

RESULT 21
US-09-345-882-4
Sequence 4, Application US/09345882
Patent No. 6393173
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
FILE REFERENCE: GENSET 031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 4

LENGTH: 6002
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 1319
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 1338
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 1944
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 3329
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 3346
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 4582
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 1107..1125
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
NAME/KEY: allele
LOCATION: 1107..1125
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 1315..1338
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 1315..1338
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID36
NAME/KEY: allele
LOCATION: 1921..1967
OTHER INFORMATION: polymorphic fragment 5-136-174 SEQ ID41
FEATURE:
NAME/KEY: allele
LOCATION: 1921..1967
OTHER INFORMATION: polymorphic fragment 5-136-174 SEQ ID62
NAME/KEY: allele

LOCATION: 3306..3352
OTHER INFORMATION: polymorphic fragment 5-143-84 SEQ ID46
FEATURE:
NAME/KEY: allele
LOCATION: 3306..3352
OTHER INFORMATION: polymorphic fragment 5-143-84 SEQ ID67
FEATURE:
NAME/KEY: allele
LOCATION: 1296..1338
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 1296..1338
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 3323..3369
OTHER INFORMATION: polymorphic fragment 5-143-101 SEQ ID45
FEATURE:
NAME/KEY: allele
LOCATION: 3323..3369
OTHER INFORMATION: polymorphic fragment 5-143-101 SEQ ID66
FEATURE:
NAME/KEY: allele
LOCATION: 4559..4605
OTHER INFORMATION: polymorphic fragment 5-148-352 SEQ ID48
FEATURE:
NAME/KEY: allele
LOCATION: 4559..4605
OTHER INFORMATION: polymorphic fragment 5-148-352 SEQ ID69
FEATURE:
NAME/KEY: misc feature
LOCATION: 442..444
OTHER INFORMATION: ATG
FEATURE:
NAME/KEY: misc feature
LOCATION: 4378..4380
OTHER INFORMATION: stop : TGA
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 4878..4883
OTHER INFORMATION: potential
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 5116..5121
OTHER INFORMATION: potential
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 5896..5901
OTHER INFORMATION: potential
FEATURE:
NAME/KEY: misc feature
LOCATION: 5981..5986
OTHER INFORMATION: 209_756
FEATURE:
NAME/KEY: misc feature
LOCATION: 391..815
OTHER INFORMATION: complement homology with EST in ref emb1:W37603
FEATURE:
NAME/KEY: misc feature
LOCATION: 453..898
OTHER INFORMATION: complement homology with EST in ref emb1:H39516
FEATURE:
NAME/KEY: misc feature
LOCATION: 818..1306
OTHER INFORMATION: complement homology with EST in ref emb1:W67770
FEATURE:
NAME/KEY: misc feature
LOCATION: 844..1303
OTHER INFORMATION: complement homology with EST in ref emb1:AA262427

FEATURE:
NAME/KEY: misc feature
LOCATION: 1351..1702
OTHER INFORMATION: complement homology with EST in ref emb1:AA485189
FEATURE:
NAME/KEY: misc feature
LOCATION: 1866..2109
OTHER INFORMATION: homology with EST in ref emb1:AA296993
FEATURE:
NAME/KEY: misc feature
LOCATION: 2181..2281
OTHER INFORMATION: homology with EST in ref emb1:T61718
FEATURE:
NAME/KEY: misc feature
LOCATION: 2253..2482
OTHER INFORMATION: homology with EST in ref emb1:AA082927
FEATURE:
NAME/KEY: misc feature
LOCATION: 2480..2842
OTHER INFORMATION: complement homology with EST in ref emb1:H38607
FEATURE:
NAME/KEY: misc feature
LOCATION: 3334..3733
OTHER INFORMATION: homology with EST in ref emb1:AA279595
FEATURE:
NAME/KEY: misc feature
LOCATION: 3631..3870
OTHER INFORMATION: complement homology with EST in ref emb1:AA169631
FEATURE:
NAME/KEY: misc feature
LOCATION: 3883..4221
OTHER INFORMATION: homology with EST in ref emb1:H08612
FEATURE:
NAME/KEY: misc feature
LOCATION: 4277..4796
OTHER INFORMATION: homology with EST in ref emb1:AA399016
FEATURE:
NAME/KEY: misc feature
LOCATION: 4516..5016
OTHER INFORMATION: homology with EST in ref emb1:AA479433
FEATURE:
NAME/KEY: misc feature
LOCATION: 5580..6002
OTHER INFORMATION: complement homology with EST in ref emb1:AA167428
US-09-345-882-4
Query Match 62.0%; Score 31.6; DB 4; Length 6002;
Best Local Similarity 89.5%; Pred. No. 1;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGA 38
DB 2056 GATGAAGAGCAGAGAGAGAGAGAGAGAGA 2093
RESULT 22
US-09-345-882-1
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bouguetel, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1

LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 72794
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele

LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140

```

: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99094..99140
: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106918..106966
: OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106918..106966
: OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108084..108130
: OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108084..108130
: OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108127..108177
: OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108127..108177
: OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
: FEATURE:

Query Match 62.0%; Score 31.6; DB 4; Length 162450;
Best Local Similarity 89.5%; Pred. No. 1.4;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0

Oy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGA 38
Db 114367 GATGAAGAAGCAGAGAGGAGGAGGAGGAGGAGA 114404

RESULT 23
US-09-817-310-1
: Sequence 1, Application US/09817310
: Patent No. 6534311
: GENERAL INFORMATION:
: APPLICANT: Stewart, Mary
: APPLICANT: Kozma, Sarah
: APPLICANT: Thomas, George
: TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
: FILE REFERENCE: 4-20971/A
: CURRENT FILING DATE: 2001-03-26
: PRIOR APPLICATION NUMBER: 09/230,247
: PRIOR FILING DATE: 1999-04-16
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2556
: TYPE: DNA
: ORGANISM: Drosophila melanogaster
US-09-817-310-1

Query Match 61.6%; Score 31.4; DB 4; Length 2556;
Best Local Similarity 77.6%; Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0

```

```

OY      2 AGGATGAAGCTGAAGAAGAGAGAGAGAGAAAGTGTGAACCCCA 50
        ||| | | | | | | | | | | | | | | | | | | | | |
DB      2161 AGGAGTGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGCTGACACAGA 2209

RESULT 24
US-09-702-705-309/c
; Sequence 309, Application US/09702705.
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702.705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 309
; LENGTH: 129
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(129)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-309

Query Match          61.2%; Score 31.2; DB 4; Length 129;
Best Local Similarity 81.8%; Pred. No. 0.94;
Matches    36; Conservative   0; Mismatches     8; Indels    0; Gaps    0;

OY      1 GAGCATGAAGCTGAAGAAGAGAGAGAGAGAGAGAAGTGTGA 44
        ||| | | | | | | | | | | | | | | | | | | | | |
DB      106 GAGGAGAGAGGTGGGAGAGAAAGAGAGAGAGAGAGAAGCTGA 63

RESULT 25
US-09-736-457-309/c
; Sequence 309, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 309
; LENGTH: 129
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:

```

DY
I GAGGATGAAGCTGAAGAGCAGGAGGAGGAGGAGAAGTGTCA 44
|||||
Dδ
106 GAGGAAGAAAGTGCGGAGGAAGAGCAGGAGGAAGAAGAAGTGA 63
|||||

RESULT 26
US-09-614-124B-309/c

```

US-09-614-124B-309
Patent No. 6630574
Sequence 309, Application US/09614124B
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darriick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 309
LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(129)
OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-309

```

Query Match	61.3%	Score 31.2;	DB 4;	Length 129;
Best Local Similarity	81.8%;	Pred. No. 0.94;		
Matches 36;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0

Dd
106 GAGGAAGAAGCTGGGAGGAGAGAGGAGGAGGAAGACGTGA 63

RESULT 27
US-09-671-325-309/C / Sequence 309 Application US/09671325
Patent No 6667134
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannon, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12 DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825

```

! NAME/KEY: misc_feature
! LOCATION: (1) .. (129)
! OTHER INFORMATION: n = A,T,C or G
US-09-671-325-309

```

Query Match	61.2%	Score 31.2;	DB 4;	Length 129;
Best Local Similarity	81.8%;	Pred. No. 0.94;		
Matches 36;	Conservative 0;	Mismatches 8.	Totals 0	0

Qy 1 GAAGATGAAGCTGAAGAGAGAGAGAGAGAGAGCTGA 44
 |||||
 Db 106 GAAGAGAGAGCTGGGAGAGAGAGAGAGAGAGAGCTGA 63
 |||||

RESULT 28
US-09-589-184-309/c
: Sequence 309, Application US/09589184
: Patent No. 6686447

```

1  APPLICANT:  Wang, Tongtong
2  APPLICANT:  Bangur, Chaltanya S.
3  APPLICANT:  Lodes, Michael A.
4  APPLICANT:  Fanger, Gary
5  APPLICANT:  Vedvick, Tom
6  APPLICANT:  Carter, Darrick
7  APPLICANT:  Reiter, Marc
8  APPLICANT:  Mannion, Jane
9  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THERAPY AND
10 FILE REFERENCE: 210121.478C8
11 CURRENT APPLICATION NUMBER: US/09/589,184
12 CURRENT FILING DATE: 2000-06-05
13 NUMBER OF SEQ ID NOS: 827
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO 309
16 LENGTH: 129
17 TYPE: DNA
18 ORGANISM: Homo sapien
19 FEATURE:
20 NAME/KEY: misc_feature
21 LOCATION: (1)...(129)
22 OTHER INFORMATION: n = A,T,C or G
23 US-09-589-184-309

```

Query Match	61.2%;	Score 31.2;	DB 4;	Length 129;
Best Local Similarity	81.8%;	Pred. No. 0.94;		
Matches	36;	Conservative	0;	Mismatches 8.

Db

106 GAGGAAGA GTGGGAGGAAGAGCGACGAAGAAGGTGA 63

RESULT 29
US-09-621-976-18731
Sequence 18731, Application US/09621976
Patent No. 663063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Ests and Encoded Human Proteins
FILE REFERENCE: GENSET, 05APR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 18731
LENGTH: 403
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-18731

Query Match 61.2%; Score 31.2; DB 4; Length 403;
Best Local Similarity 81.8%; Pred. No. 1;
Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGA 44
DB 343 GAGGAAGAGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGTGA 384

RESULT 30

US-09-621-976-18711
Sequence 18711, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Joberl, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18711
LENGTH: 427
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 72,215,229
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18711

Query Match 61.2%; Score 31.2; DB 4; Length 427;
Best Local Similarity 81.8%; Pred. No. 1;
Matches 36; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGA 44
DB 343 GAGGAAGAGGTGGGAGAGAGAGAGAGAGAGAGAGAGAGTGA 386

Search completed: February 29, 2004, 22:26:08
Job time : 65.5 secs

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```
/ APPLICANT: Jiang, Bo
/ APPLICANT: Hu, Wengf
/ APPLICANT: Tishkoff, Daniel
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Eroshkin, Alexey M
/ APPLICANT: Lemieux, Sebastien M
/ TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
/ FILE REFERENCE: 10182-018-999
/ CURRENT APPLICATION NUMBER: US/10/128,714
/ CURRENT FILING DATE: 2002-04-23
/ PRIOR APPLICATION NUMBER: US 60/285,697
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: US 60/287,066
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: US 60/295,890
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US 60/303,899
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/316,362
/ PRIOR FILING DATE: 2001-08-31
/ NUMBER OF SEQ ID NOS: 8603
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 7204
/ LENGTH: 2367
/ TYPE: DNA
/ ORGANISM: Aspergillus fumigatus
US-10-128-714-7204
```

```
Query Match          70.6%; Score 36; DB 14; Length 2367;
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 44
    |||||
Db 2314 GAGGAGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 2357
```

```
RESULT 12
US-10-128-714-204
/ Sequence 204, Application US/10128714
/ Publication No. US20030119013A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Bo
/ APPLICANT: Hu, Wengf
/ APPLICANT: Tishkoff, Daniel
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Eroshkin, Alexey M
/ APPLICANT: Lemieux, Sebastien M
/ TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
/ FILE REFERENCE: 10182-018-999
/ CURRENT APPLICATION NUMBER: US/10/128,714
/ CURRENT FILING DATE: 2002-04-23
/ PRIOR APPLICATION NUMBER: US 60/285,697
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: US 60/287,066
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: US 60/295,890
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US 60/303,899
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/316,362
/ PRIOR FILING DATE: 2001-08-31
/ NUMBER OF SEQ ID NOS: 8603
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 204
/ LENGTH: 4238
/ TYPE: DNA
/ ORGANISM: Aspergillus fumigatus
US-10-128-714-204
```

```
Query Match          70.6%; Score 36; DB 14; Length 4238;
```

```
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 44
    |||||
Db 3314 GAGGAGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 3357
```

```
RESULT 13
US-10-128-714-5204
/ Sequence 5204, Application US/10128714
/ Publication No. US20030119013A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Bo
/ APPLICANT: Tishkoff, Daniel
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Eroshkin, Alexey M
/ APPLICANT: Lemieux, Sebastien M
/ TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
/ FILE REFERENCE: 10182-018-999
/ CURRENT APPLICATION NUMBER: US/10/128,714
/ CURRENT FILING DATE: 2002-04-23
/ PRIOR APPLICATION NUMBER: US 60/285,697
/ PRIOR FILING DATE: 2001-04-23
/ PRIOR APPLICATION NUMBER: US 60/287,066
/ PRIOR FILING DATE: 2001-04-27
/ PRIOR APPLICATION NUMBER: US 60/295,890
/ PRIOR FILING DATE: 2001-06-05
/ PRIOR APPLICATION NUMBER: US 60/303,899
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: US 60/316,362
/ PRIOR FILING DATE: 2001-08-31
/ NUMBER OF SEQ ID NOS: 8603
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 5204
/ LENGTH: 4367
/ TYPE: DNA
/ ORGANISM: Aspergillus fumigatus
US-10-128-714-5204
```

```
Query Match          70.6%; Score 36; DB 14; Length 4367;
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 44
    |||||
Db 3314 GAGGAGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 3357
```

```
RESULT 14
US-10-424-599-139707
/ Sequence 139707, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovallik David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 139707
/ LENGTH: 1012
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_97163C.1
US-10-424-599-139707
```

[illegible]

Query Match	68.2%	Score 34.8	DB 12	Length 1537	
Best Local Similarity	84.8%	Pred. No. 0.089	7	Indels 0	Gaps 0
Matches 39, Conservative					

Db

Oy

1 GAGGATGAACCTGAAAGAGGAGGAGGAGGGAGGAGGAGGAGAAGGTGTAAAC 46
| | | | |
583 GAGATGAGATTATGTCGAGGAGGAGGAGGAGGAGTGTGTTTGACC 62

```

RESULT 16
US-09-864-408A-3111
; Sequence 3111, Application US/09864408A
; Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: leach, Martin D.
APPLICANT: Shlensky, Richard A.
TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encc
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3111
LENGTH: 392
TYPE: DNA
ORGANISM: Homo sapiens
US-09-864-408A-3111

```

Query Match:	67.5%	Score	34.4;	DB	11;	Length	392;
Best Local Similarity:	86.4%;	Pred.	No. 0.12;				
Matches	38;	Conservative	0;	Mismatches	6;	Gaps	0;
OY	1	GAGGATGAACCTGAAGAGCAGAGGAGGAGGAGAAGTGTGA	44				
Db	85	GAAATGAGGAGGAAGAGAGGAGGAGGAGGAGAAGCGGAGA	128				

Query Match	Score	DB	Length	Score
Best Local Similarity	86.4%	Pred. No. 0.12		
Matches	38	Conservative	0	Mismatches
			6	Indels
			0	Gaps

QY 1 GAGGATGAAGTGAAGAGGAGGAGGAGCGACGGAAAGCTGTGA 44
 |||||
Db 3109 GAGGATGAAGATGAAGAGGAGGAGGAGCGAGCGAAGATTGAGACGA 3157

```

RESULT 18
US-09-844-864-12
; Sequence 12, Application US/09844864
; Patent No. US20020042926A1
; GENERAL INFORMATION:
; APPLICANT: Matzok, Martin
; APPLICANT: Ren, Yongsheng
; APPLICANT: Wu, Xuemei
; TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
; PCT NO.: P01925US2 / 09807797 / OTA 99-48
; CURRENT APPLICATION NUMBER: US/09/844, 864
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/106,020
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: PCT/US99/25209
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-844-864-12

```

	Query Match	66.3%;	Score 33.8;	DB 9;	length 182;
	Best Local Similarity	84.4%;	Pred. No. 0.19;		
	Matches	38;	Conservative	0;	Mismatches 7; Indels 0; Gaps 0
OY	1	GAGGATGAAGCTGACAGAGCGAGCGAGCGAAGAAGTGTGAA	45		
Dd	36	GAAGATCAAGAGGAGAGGAGGAGGAGGAGGAGGAGGATGAA	80		


```

: APPLICANT: Slater, Steven C.
: APPLICANT: Goldman, Barry S.
: APPLICANT: Chen, Xianfeng
: TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
: TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
: FILE REFERENCE: 38-10(52052)B
: CURRENT APPLICATION NUMBER: US/10/369,493
: CURRENT FILING DATE: 2003-02-28
: PRIOR APPLICATION NUMBER: US 60/360,039
: PRIOR FILING DATE: 2002-02-21
: NUMBER OF SEQ ID NOS: 47374
: SEQ ID NO 27799
: LENGTH: 3401
: TYPE: DNA
: ORGANISM: Neurospora crassa
: US-10-369-493-27799

Query Match      66.3%; Score 33.8; DB 15; Length 3401;
Best Local Similarity 84.4%; Pred. No. 0.18;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

: APPLICANT: Warner-Lambert Company
: APPLICANT: Lee, Kevin
: APPLICANT: Dixon, Alistair
: APPLICANT: Brooksbank, Robert
: APPLICANT: Pimock, Robert
: TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
: FILE REFERENCE: WL-A-018201
: CURRENT APPLICATION NUMBER: US/10/205,194
: CURRENT FILING DATE: 5200-07-24
: PRIOR APPLICATION NUMBER: GB 0118354.0
: PRIOR FILING DATE: 2001-07-27
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 145
: LENGTH: 2981
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: OTHER INFORMATION: RNA1 homolog
: US-10-205-194-145

Query Match      65.5%; Score 33.4; DB 14; Length 2981;
Best Local Similarity 78.4%; Pred. No. 0.24;
Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wenheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aeomica-X-1

: APPLICANT: Slater, Steven C.
: APPLICANT: Goldman, Barry S.
: APPLICANT: Chen, Xianfeng
: TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
: TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
: FILE REFERENCE: 38-10(52052)B
: CURRENT APPLICATION NUMBER: US/10/369,493
: CURRENT FILING DATE: 2003-02-28
: PRIOR APPLICATION NUMBER: US 60/360,039
: PRIOR FILING DATE: 2002-02-21
: NUMBER OF SEQ ID NOS: 47374
: SEQ ID NO 27799
: LENGTH: 3401
: TYPE: DNA
: ORGANISM: Neurospora crassa
: US-10-369-493-27799

Query Match      66.3%; Score 33.8; DB 15; Length 3401;
Best Local Similarity 84.4%; Pred. No. 0.18;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

: APPLICANT: Warner-Lambert Company
: APPLICANT: Lee, Kevin
: APPLICANT: Dixon, Alistair
: APPLICANT: Brooksbank, Robert
: APPLICANT: Pimock, Robert
: TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
: FILE REFERENCE: WL-A-018201
: CURRENT APPLICATION NUMBER: US/10/205,194
: CURRENT FILING DATE: 5200-07-24
: PRIOR APPLICATION NUMBER: GB 0118354.0
: PRIOR FILING DATE: 2001-07-27
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 145
: LENGTH: 2981
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: OTHER INFORMATION: RNA1 homolog
: US-10-205-194-145

Query Match      65.5%; Score 33.4; DB 14; Length 2981;
Best Local Similarity 78.4%; Pred. No. 0.24;
Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wenheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aeomica-X-1

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us-09-692-077d-2_copy_880_930.rnpb

[illegible]

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TYPE: Unk
ORGANISM: Homo sapiens
FEATURE INFORMATION: MAP to AC004687.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED HIT: P51450, EVALU8 7.0e-02
OTHER INFORMATION: SWISSPROT HIT: A6014512.1, EVALU8 1.00e-38
OTHER INFORMATION: NT HIT: A8014512.1, EVALU8 2.00e-38
OTHER INFORMATION: EST_HUMAN HIT: A1653251.1, EVALU8 2.00e-38
US-09-864-761-23094
Query_Match 65.1%; Score 33.2; DB 9; Length 193;
Best_Local Similarity 92.1%; Pred. Mismatches 3; Indels 0; Gaps 0
Matches 35: Conservative
2 AGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGG 120
83 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
RESULT 24
US-09-918-995-27029
; Sequence 27029, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION.

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[illegible]

RESULT 25
US-09-864-761-6378 Application US/09864761
Sequence 6378
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Katz, David R.
APPLICANT: Hatzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aesomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
David R.
Bank, 121

Genetic ACID PROBES USEFUL FOR C

GENERAL: Penn, David R.
APPLICANT: Rank, David
APPLICANT: Manzel, David

APPLICANT: HUMAN GENOME ANALYSIS
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: NEOMICA-X-2
US/10/029,386

FILE REFERENCE: 2001-12-20
CURRENT FILING DATE: 34288
Engine ver. 1.1

CURRENT OF SEQ
NUMBER OF ANNO
SOFTWARE: 18468

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' SEQ ID NO 1000
' LENGTH: 150
' TYPE: DNA
' name: haplenb

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ORGANISM: HOMO SAPIENS
MAP TO AC011400.4, SIGNAL = 7.7
FEATURE: EXPRESSED IN BONE MARROW
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.6

OTHER INFORMATION:		Length	127
' OTHER INFORMATION: 18468			
' OTHER INFORMATION: 18468			
US-10-029-386-18468	Score 32.8;	DB 14;	
CA 3%;	No. 0.38;	Indels	Gaps
			0;

Query Match	Similarity	Conservative	Pred: matches	Mismatches
Best Local	84.1%	0	0	0

[illegible]

QY 29
pb

RESULT 30 44-146 44-146 US/09728444

US-09-728-444
Sequence 146, Application
; Patent No. US20020161207A1

APPLICANT: Zambronicz, Brian
APPLICANT: Arthur T.

APPLICANT: Santos, No. US20020202020
TITLE OF INVENTION: and Mutant Cells
OF INVENTION: 0100-USA

TITLE OF INVENTION: LEX-VISOR
FILE REFERENCE NUMBER: US 09/122,000
FILING DATE: 2000-11-30
PRIORITY DATE: 2000-11-30
CROSS REFERENCE TO RELATED APPLICATIONS: US 60/168,360
CLASSIFICATION: 359/800,000

CURRENT FILING NUMBER: 2001-01-01
 CURRENT APPLICATION NUMBER: 1999-12-01
 PRIOR FILING DATE: 1999-12-01
 PRIOR FILING NOS: 1206
 Version 4.0

NUMBER OF SEQ ID FOR WINDOWS
SOFTWARE: FASTSEQ
ST NO 146

SEQ ID NO: 223
LENGTH: 223
TYPE: DNA
ORGANISM: Mus musculus

```

ORGANISM:
FEATURE: misc feature
NAME/KEY: (1) ... (223)

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LOCATION: \1\	n = 1	DB 9:	Length 223:	Gaps
OTHER INFORMATION: 146	Score 32.8:	0 37:	0 0:	0
00-728-444-146				

Query	Local Similarity	Derivative	Mismatches
US-05-72	64.3%	Pred. No. 0.57	7; Inver-
Match	84.1%	0; Mismatches	
AGAGAGTGTGA	44		

[illegible]

QY
14 GAGGAGGAAGAAGAGGAGGAGGAG

Search completed: February 29, 2004, 22:00
Job time 208 secs